

# SEARCH REQUEST FORM

Scientific and Technical Information Center

Access DB#

49160

Requester's Full Name: \_\_\_\_\_ Examiner #: \_\_\_\_\_ Date: \_\_\_\_\_  
 Art Unit: \_\_\_\_\_ Phone Number 30 \_\_\_\_\_ Serial Number: \_\_\_\_\_  
 Mail Box and Bldg/Room Location: \_\_\_\_\_ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

\*\*\*\*\*  
 Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

## STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: _____	NA Sequence (#) _____	STN _____
Searcher Phone #: _____	AA Sequence (#) <u>1+1</u>	Dialog <u>Reverse to N4</u>
Searcher Location: _____	Structure (#) _____	Questel/Orbit: _____
Date Searcher Picked Up: <u>8/17/01</u>	Bibliographic _____	Dr. Link _____
Date Completed: <u>8/19/01</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems <u>01</u>
Clencal Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: _____	Other _____	Other (specify) _____

OM of: US-09-457-066-2\_COPY\_210\_345 to: EST:\* out\_format : pfs

Date: Aug 18, 2001 4:10 AM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

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-MODE=framer-p2n.model -DEV-xmlp
-Q=/cgn2.1/USPTO_spool/US09457066/runat_17082001_083144_25044/app-query.fasta_1.207
-DB=EST -QFMT=fastap -SUFFIX=est -GAPOP=12.000 -GAPEXT=4.000
-MINWATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -OGAPOP=4.500
-OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -EGAPOP=6.000
-EGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM-ext -MINLEN=0
-MAXLEN=200000000 -USPR=US09457066.@CGN1_1.2722 -NCPU=6
-ICPU=3 -LONGLOG -NO_XLPXY -WAIT -THREADS=1
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Search information block:

Query: US-09-457-066-2\_COPY\_210\_345

Query length: 136

Database: EST:\*

Database sequences: 10228115

Search length: 431459454

Search time (sec): 1369.120000

score\_list:

Sequence	Strd Orig	25score	EScore	Len	Documentation
gb_est102.BG609411	+	708.00	1373.56	556	..
gb_est81.BE958470	+	705.00	1368.32	523	! BG609411 323251 MARC IPIG Sus s
gb_est82.BE021679	+	697.00	1352.66	523	! BE958470 601644787F1 NIH_MGC_58
gb_est83.BF151355	+	663.00	1285.31	564	! BF021679 uv50f05.y1 NCI_CGAP.Lu
gb_est83.BF102859	+	663.00	1285.31	564	! BF151355 ua15b12.y1 NCI_CGAP.Ma
gb_est83.BF102859	+	622.00	1200.76	851	! BF102859 601646827F1 NIH_MGC_60
gb_est83.BF102859	+	606.00	1168.73	910	! BG243001 602355974F1 NCI_CGAP.M
gb_est82.BF011835	+	587.00	1138.92	447	! BF011835 us37d10.y1 Soares.NHEB
gb_est28.AL047637	+	568.00	1105.72	304	! AL047637 DKFZP58630421.r1 586 C
gb_est91.BF670092	+	538.50	1036.96	874	! BF670092 602119417F1 NIH_MGC_58
gb_est82.BF031624	+	523.00	1005.78	950	! BF031624 601558104F1 NIH_MGC_58
gb_est97.BF118707	+	507.00	974.26	968	! BF118707 602348280F1 NIH_MGC_90
gb_gss3.CNS024MX	-	439.50	843.12	877	! AL180978 Tetraodon nigroviridis
gb_gss3.CNS024MX	-	381.00	728.29	902	! BF163629 601769732F1 NCI_CGAP.L
gb_htc.AK003359	+	345.50	651.63	1796	! AK003359 Mus musculus 18 days
gb_est15.A1020581	+	327.00	633.20	324	! A1020581 ua96c08.r1 Soares.mamm
gb_est73.BE374398	+	323.50	621.41	521	! BE374398 601229756F1 NCI_CGAP.M
gb_est44.AW210331	+	283.00	542.32	511	! AW210331 ui53f09.y1 Rashbass mc
gb_est11.AA759138	-	254.00	487.45	425	! AA759138 ah78f03.s1 Soares_test
gb_est20.A1470494	+	246.00	473.69	354	! A1470494 t144e11.x1 Soares.NSF
gb_est97.BG173847	+	228.50	428.34	1029	! BG173847 602333906F1 NCI_CGAP.L
gb_gss4.CNS0458A	-	217.50	406.73	1036	! AL304867 Tetraodon nigroviridis
gb_est53.AW688905	+	215.50	409.21	560	! AW688905 ESTR80981 MAGE resequ
gb_est83.BF117246	+	214.00	421.77	126	! BF117246 uz07a06.y1 NCI_CGAP.Ma
gb_est84.BF167693	+	211.50	406.65	337	! BF167693 xm47g09.x1 Soares_NHCE
gb_est15.A1024617	+	210.00	402.23	389	! A1024617 ov52f10.x1 Soares_test
gb_est84.BF143048	+	168.00	312.96	765	! BF143048 601788733F1 NCI_CGAP.L
gb_est110.W21436	+	157.00	297.86	412	! W21436 zb52a06.r1 Soares_fetal
gb_est8.AA488780	+	152.50	290.45	360	! AA488780 aa54c10.r1 NCI_CGAP.GC
gb_est49.AW582560	+	146.00	284.26	192	! AW582560 RC1-SF0278-080100-011
gb_est72.BE289243	+	135.00	250.06	649	! BE289243 601092806F1 NCI_CGAP.M
gb_est84.BF137533	+	134.50	245.95	877	! BF137533 601780533F1 NCI_CGAP.L
gb_est42.AW052200	+	128.00	246.57	243	! AW052200 w787c04.x1 Soares_NSF
gb_est81.BE937452	+	116.50	228.72	0.0013	! BE937452 RC1-SF0278-310800-019
gb_est89.BF551964	+	110.50	205.34	475	! BF551964 UI-R-C22p-g-09-0-UI
gb_est95.BG080810	+	110.00	204.85	0.0272	! BG080810 QV4-GN0314-281100-607
gb_est100.BG387377	+	110.00	199.78	0.0522	! BG387377 602456142F1 NIH_MGC_15
gb_est80.BE844375	+	108.50	196.76	0.0768	! BE844375 EST119 Apis mellifera
gb_est4.AA240232	+	107.00	199.54	0.0538	! AA240232 my24b02.r1 Barstead mc
gb_est83.BF130765	+	106.00	190.68	0.1676	! BF130765 601818408F1 NIH_MGC_58
gb_est83.BF128614	+	105.50	194.61	0.1013	! BF128614 601810869F1 NIH_MGC_48
gb_est49.AW634441	+	105.50	194.49	0.1028	! AW634441 b120g09.w1 Blackshear

gb\_est97.BG167387 + 105.50 188.30 0.2273 954 ! BG167387 602342635F1 NIH\_MGC

gb\_est93.BF876874 + 105.00 195.92 0.0855 417 ! BF876874 PM4-ETU154-151100-0

gb\_est48.AW555889 - 105.00 192.67 0.1297 570 ! AW555889 L0260G12-3 Mouse Ne

gb\_est26.A1893253 - 104.50 187.03 0.2676 893 ! A1893253 me29e08.y1 Soares m

seq\_name: gb\_est102.BG609411

seq\_documentation\_block:

LOCUS BG609411 556 bp mRNA EST 17-APR-2001

DEFINITION 323251 MARC IPIG Sus scrofa cDNA 5', mRNA sequence.

ACCESSION BG609411

VERSION BG609411.1 GI:13659390

KEYWORDS EST.

SOURCE pig.

ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 556)

AUTHORS Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keele,J.W.

TITLE Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine

JOURNAL Unpublished (2000)

COMMENT Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt\_trimmed with phred v0.980904.e. Vector identified by cross\_match with the -minscore 18 and -minmatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCCTCCAGTCACGACG

Plate: 98 row: P column: 8

Seq primer: ATTAGGTGACACTATAG.

Location/Qualifiers

1..556

/organism="Sus scrofa"

/db\_xref="taxon:9823"

/clone\_lib="MARC IPIG"

/tissue\_type="pooled"

/lab\_host="DH10B"

/note="Vector: PCMV SPORT6; Site\_1: XbaI; Site\_2: XhoI;

Library made from pooled tissue from day 11, 13, 15, 20,

and 30 embryos."

BASE COUNT 139 a 153 c 141 g 123 t

ORIGIN

alignment\_scores:

Quality: 708.00 Length: 130

Ratio: 5.488 Gaps: 0

Percent Similarity: 99.231 Percent Identity: 97.692

alignment\_block:

US-09-457-066-2\_COPY\_210\_345 x BG609411

Align seg 1/1 to: BG609411 from: 1 to: 556

1 LeuAspLeuGluAspLeuTyrArgProThrTrpClnLeuLeuGlyLysAl 17

167 CTGACTTAGAAGATCTATACAGGCCAACCTGGCACTGTCGCAAGGC 216

17 apbeValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThrG 34

217 TTTTGTTCGGAAGAAATCCAGAGTGGTGGATCTGAACCTTCTCAAG 266

34 luGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerIle 50

267 AACAACTGAGGCTATACAGCTGACCCCTAGGAACTTTTCACTGCTATC 316

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51  ArgGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeuLe 67
|||||
317 AGGGAAGAGCTGAAGAGAAGACAGACCATCTTCTGGCCAGGCTGCCCTCT 366
|||||
67  uValLysArgCysGlyGlyAsnCysAlaCysLeuHisAsnCysAsnG 84
|||||
367 CGTCAAGCGTTGTGGGGGAACTGTGCTGCTGATGCACACCTGCAATG 416
|||||
84  luCysGlnCysValProSerLysValThrLysLysTyrHisGluValLeu 100
|||||
417 AGTGTCAAGTGTCTCCCGCAGCAAGTACCAAGAAATATCAGAGGTCCTT 466
|||||
101 GlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThrAs 117
|||||
467 CAGTTGAGACCCCAAGACAGGTGTCCGGGGGCTGCACAAAGTCCCTCACCGA 516
|||||
117 pValAlaLeuGluHisGluGluCysAspCysValCys 130
|||||
517 CGTGGCCCTGGACACCAAGAGGAGTGTGACTGCGTGTGC 556
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seq\_name: gb\_est81:BE958470

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seq_documentation_block:
LOCUS BE958470 523 bp mRNA EST 04-OCT-2000
DEFINITION 601644787F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930045 5',
mRNA sequence.
ACCESSION BE958470
VERSION BE958470.1 GI:10569175
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CNA Library Preparation: CLONETECH Laboratories, Inc.
CNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM763 row: m column: 22
High quality sequence start: 2
High quality sequence stop: 513.
Location/Qualifiers
1..523
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3930045"
/clone_lib="NIH_MGC_56"
/tissue_type="primitive neuroectoderm"
/lab_host="DH10B (T1 phage-resistant)"
/notice="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccctcgcc); Site_2: SfiI (ggccattggcc);
Double-stranded cDNA was prepared from cell line RNA.
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CAGGCGCATATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCCGAGCGCGACATG-dt(30)BN-3'
(where B = A, C, G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
BASE COUNT 147 a 118 c 129 g 128 t 1 others
ORIGIN

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FEATURES  
source

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alignment_scores:
Quality: 705.00 Length: 136
Ratio: 5.261 Gaps: 0
Percent Similarity: 98.529 Percent Identity: 97.794

alignment_block:
US-09-457-066-2_COPY_210_345 x BE958470 ..
Align seg 1/1 to: BE958470 from: 1 to: 523
1 LeuAspLeuGluAspLeuTyrArgProThrTrpGlnLeuGlyLysAl 17
:::|||||
103 GTGGACTTAGAAGATCTATATAGCCAACTTGGCAACTTCTTGGCAAGC 152
|||||
17 aPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThrG 34
|||||
153 TTTCTGTTTTTCGGAAGAAATCCAGAGTGGTGATCTGAACCTTCTAACAG 202
|||||
34 luGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerIle 50
|||||
203 AGGAGGTAAGATTATACAGCTGCACACCTCGTAACCTTCTCAGTGTCCATA 252
|||||
51 ArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeuLe 67
|||||
253 AGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCTCT 302
|||||
67 uValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsnG 84
|||||
303 GGTAAACGCTGTGTGGGAACCTGTGCGCTGNTGTCTCCACAAATTGCAATG 352
|||||
84 luCysGlnCysValProSerLysValThrLysLysTyrHisGluValLeu 100
|||||
353 AATGTCAATGTGTCCAAAGCAAGTTACTAAAAAATACCACGAGTCTCTT 402
|||||
101 GlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThrAs 117
|||||
403 CAGTTGAGACCCCAAGACCGGTGTGAGGGGATTCACAAATCACTCACCGA 452
|||||
117 pValAlaLeuGluHisGluGluCysAspCysValCysArgGlySerT 134
|||||
453 CGTGGC.CTGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCA 501
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134 hrGlyGly 136
502 CAGGAGGA 509

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seq\_name: gb\_est82:BF021679

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seq_documentation_block:
LOCUS BF021679 523 bp mRNA EST 29-DEC-2000
DEFINITION uy50f05.y1 NCI-CGAP_Lu30 Mus musculus cDNA clone IMAGE:3663009 5',
similar to TR:Q9QY71 Q9QY71 FALLOTEIN.; mRNA sequence.
ACCESSION BF021679
VERSION BF021679.1 GI:10753011
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CNA Library Preparation: Life Technologies, Inc.
CNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml

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MGI:1423777
Seq primer: -40RP from Gibco
High quality sequence stop: 452.

FEATURES
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            /strain="Czech II"
            /db_xref="taxon:10090"
            /clone="IMAGE:3663009"
            /clone_lib="MCL_CGAP_Lu30"
            /tissue_type="tumor, metastatic to mammary"
            /lab_host="DH10B"
            /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; transgenic model WNT-1, expression driven by MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. NIH"
            Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT      143 a   116 c   139 g   125 t
ORIGIN

alignment_scores:
    Quality: 697.00      Length: 136
    Ratio: 5.201      Gaps: 0
    Percent Similarity: 98.529      Percent Identity: 88.971

alignment_block:
US-09-457-066-2_COPY_210_345 x BF021679 ..

Align seg 1/1 to: BF021679 from: 1 to: 523

1  LeuAspLeuGluAspLeuTyArgProThrTrpGlnLeuLeuGlyLysAl 17
   ::::::::::::::::::::::::::::::::::::::::::::::::::::
116 GTGGAGCTTGGACAGCCTCTACAAGCCACATGGCAGCTTTTGGGCAAGC 165

17  aPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThrG 34
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::
166 TTTCTCTGATGGGAAAAAAGCAAGAGTGGTGAATCTGAATCTCTCTAAAGG 215

34  luGluValArgLeuTySerCysThrProArgAsnPheSerValSerIle 50
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::
216 AAGAGTAAACTCTACAGCTGCACACCCGCACTTCTCAGTGTCCATA 265

51  ArgGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeuLe 67
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::
266 CGGGAAGAGCTAAAGAGGACAGATACCATATTTCTGGCCAGGTTGTCTCT 315

67  uValLysArgCysGlyValAsnCysAlaCysCysLeuHisAsnCysAsnG 84
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::
316 GGTCAAGCGCTGTGAGGAAATGTGCCTGTGTCTCCATATTTCAATG 365

84  luCysGlnCysValProSerLysValThrLysLysTyrHisGluValLeu 100
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::
366 AATGTCAGTGTCTCCACGTAAGTTACAAAAGATACCATGAGGTCCTT 415

101 GlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThrAs 117
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::
416 CAGTTTGAGACCAAAACTGGAGTCAAGGATGTGCATAAGTCACTCAC 465

117 pValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySerT 134
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::
466 TGTGGCTCTGGAACACCCACGAGGAATGTCACTGTGTGTAGAGGAAACG 515

134 hrGlyGly 136
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516 CAGGAGGG 523

seq_name: gb_est84:BF151355

seq_documentation_block:
LOCUS      BF151355      564 bp      mRNA      EST      29-DEC-2000
DEFINITION  u215b12.y1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3669119 5'

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similar to TR:Q9QY71 Q9QY71 FALLOTEIN. ;, mRNA sequence.  
 BF151355  
 VERSION BF151355.1 GI:11032750  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 564)  
 REFERENCE NCI-CCAG <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 TITLE Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapsb-r@mail.nih.gov  
 Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys  
 CDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone Distribution: NCI-CCAG clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
[image.llnl.gov/image/html/iresources.shtml](http://image.llnl.gov/image/html/iresources.shtml)

MGI:1429887
Seq primer: -4ORP from Gibco
High quality sequence stop: 436.
Location/Qualifiers
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/strain="C57/B6"
/db_xref="taxon:10090"
/clone_image="IMAGE:3669119"
/clone_lib="MCL_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/note="Organ; mammary; Vector: pCMV-SPORT6; site_1: Salt;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"
157 a   130 c   140 g   137 t
BASE COUNT
ORIGIN

```

alignment_scores:
  Quality: 663.00      Length: 133
  Ratio: 5.140         Gaps: 0
  Percent Similarity: 96.992  Percent Identity: 87.218

alignment_block:
  US-09-457-066-2_COPY_210_345 x BF151355  . .
  Align seg 1/1 to: BF151355 from: 1 to: 564

1  LeuAspLeuGluAspLeuTyArgProThrTrpGlnLeuLeuGlyLysAl 17
   : : : : : : : : : : : : : : : : : : : : : : : :
163 GTGGACTTGGACAGCCCTCTACAAGCCAACTGGCAGCTTTTGGCAAGGC 212

17  aPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThrG 34
   : : : : : : : : : : : : : : : : : : : : : : : :
213 TTTCTCTGTATGGGAAAAAAGCAAGTGGTGAATCTGAATCTCTCTCAAGG 262

34  lucluValArgLeuTyArgSerCysThrProArgAsnPheSerValSerIle 50
   : : : : : : : : : : : : : : : : : : : : : : : :
263 AAGAGGTAAACCTCTACAGCTGCACACCCCGGAATCTCTAGTGCCATA 312

51  ArgGluGluLeuLysArgThrAspThrIlePheTppProGlyCysLeuLe 67
   : : : : : : : : : : : : : : : : : : : : : : : :
313 CGGGAAGAGCTAAAGAGGACAGATACCATATTTCTGCCAGGTTGTCTCT 362

67  uValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsnG 84
   : : : : : : : : : : : : : : : : : : : : : : : :

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seq_name: gb_est84:BF151355
seq_documentation_block:
LOCUS      BF151355      564 bp      mRNA      EST      29-DEC-2000
DEFINITION u215b12.y1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3669119 5'
```

```
363 GGTCAAGCGCTGGAGGAATTTGCTGTTCTCCATAATTGCAATG 412
84 luCysGlnCysValProSerLysValThrLysLysTyrHisGluValLeu 100
|||||
413 AATGTCAGTGTCTCCACACCAAGTTTACAAAAAGTACCATGAGGTCCTT 462
|||||
101 GlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThrAs 117
|||||
463 CAGTTGAGACCAAACTCGAGTCAAGGAGTGCATATAAGTACTCAATGA 512
|||||
117 pValAlaLeuGluHisHisGluCysAspCysValCysArgGlySer 133
|||||
513 TGTGCTCTTGAACACCAACAGGAGTGTGCTGAGAGGGAAC 561
|||||
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seq\_name: gb\_est83:BF102859

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seq_documentation_block:
LOCUS      BF102859      851 bp      mRNA      EST      19-OCT-2000
DEFINITION 601646827F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4073095 5',
            mRNA sequence.
ACCESSION  BF102859
VERSION     BF102859.1 GI:10885385
KEYWORDS   EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 851)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTF
            cDNA Library Preparation: CLONETECH Laboratories, Inc.
            DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: L1CM921 row: f column: 08
            High quality sequence stop: 529.
```

FEATURES

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Source
Location/Qualifiers
1..851
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4073095"
/clone_lib="NIH_MGC_60"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site_1: SfII (ggcgcctggcc); Site_2: SfII (ggcattatggcc
); Double-stranded cDNA was prepared from cell line RNA.
5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CAGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATCTAGAGCGGAGCGGCACATG-dt(30)BN-3'
(where B = A, C, G, or T). Average
insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
Library."
BASE COUNT 234 a 169 c 238 g 210 t
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alignment\_scores:

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Quality: 622.00 Length: 138
Ratio: 4.712 Gaps: 4
Percent Similarity: 95.652 Percent Identity: 93.478
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alignment\_block:

US-09-457-066-2\_COPY\_210\_345 x BF102859

Align seg 1/1 to: BF102859 from: 1 to: 851

```
1 LeuAspLeuGluAspLeuTyrArgProThrTrpGlnLeuLeuGlyLysAl 17
|||||
149 TTGGACTTAGAAGATCATATAGGCCAACTTGGCAACTTCTTGGCAAGGC 198
|||||
17 aPheVal.PheGlyArgLysSerArgValValAspLeuAsnLeuLeuThr 33
I ::|
199 T...TTGTTTTGGAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTTAACA 245
|||||
34 GluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerIl 50
|||||
246 GAGGAGGTAAGATTATACAGCTGCACACCTCGTAACCTTCTCAGTGTCCAT 295
|||||
50 eArgGluGluLeuLysArgThrAspThrIlePheThrProGlyCysLeuL 67
|||||
296 AAGGAAGAACTAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCTCC 345
|||||
67 euValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsn 83
|||||
346 TGGTTAAACGCTGTGGTGGGAACGTGCTG. TGTCTCCACAATTGCAAT 394
|||||
84 GluCysGlnCysValProSerLysValThrLysLysTyrHisGluValLe 100
|||||
395 GAATGTCAATGTGTCCCAAGCAAGTTACTAAAAAATACCAAGAGTCT 444
|||||
100 uGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThra 117
|||||
445 TCAGTTAGACCAAGAACCGGTGTCAGGGGATG.CACAAATCACTCACCG 493
|||||
117 spValAlaLeu.GluHisHisGluGluCysAspCysValCysArgGlyse 133
|||||
494 ACCTG...GCCTGAGCACCATGAGGAGTGTGCTGTCGAGGGAGC 540
|||||
133 rThrGlyGly 136
:|||||
541 CACAGGGGGGA 550
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seq\_name: gb\_est98:BG243001

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seq_documentation_block:
LOCUS      BG243001      910 bp      mRNA      EST      13-FEB-2001
DEFINITION 602355974F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4483938 5',
            mRNA sequence.
ACCESSION  BG243001
VERSION     BG243001.1 GI:12752725
KEYWORDS   EST.
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
REFERENCE   1 (bases 1 to 910)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/
JOURNAL    National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT     Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10323 row: d column: 19
            High quality sequence stop: 690.
```

FEATURES

```
Location/Qualifiers
1..910
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4483938"
```

BASE COUNT 242 a 220 c 250 g 198 t  
ORIGIN

/clone\_lib="NCI\_CGAP\_Mam1"  
/tissue\_type="tumor, biopsy sample"  
/dev\_stage="3 months, virgin"  
/lab\_host="DH10B"  
/note="Organ: mammary; Vector: pCMV-SPORT6; Site\_1: SalI;  
Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Library constructed by Life Technologies. Investigator  
providing samples: Gilbert Smith, NIH"

alignment\_scores:  
Quality: 606.00 Length: 136  
Ratio: 4.591 Gaps: 0  
Percent Similarity: 97.059 Percent Identity: 87.500

alignment\_block:  
US-09-457-066-2\_COPY\_210\_345 x BG243001 ..

Align seg 1/1 to: BG243001 from: 1 to: 910

1 LeuAspLeuGluAspLeuTyrArgProThrTrpGlnLeuLeuGlyLysAl 17  
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
108 GTGAGCTGGGACAGCCTCTACAGCCACATGGCAGCT.TTGGGCAAGGC 156

17 apheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThrG 34  
|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
157 TTTCTCTGTATGGGAAAAAAGCAAGTGGTGAATCTGAATCTCTCTCAAGG 206

34 luGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerIle 50  
|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
207 AAGAGGTAATAACTTACAGCTGCACACCCCGGAATCTCTCAGTGTCCATA 256

51 ArgGluGluLeuLysThrArgThrAspThrIlePheThrProGlyCysLeu 67  
|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
257 CGGAAGAGCTAAGAGAGACAGATACCATATCTGGCCAGGTGTCTCTCT 306

67 uValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsnG 84  
|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
307 GGTCAAGCGCTGTGGAGGAAA.TGTGCTGTGTCTCCATAATTCGAATG 355

84 luCysGlnCysValProSerLysValThrLysLysTyrHisGluValLeu 100  
|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
356 AATCTCAGTGTGTCCCGTAAAGTTACAAAAAGTACCATGAGGTCTCT 405

101 GlnLeuArgProLysThrGlyValArgGlyLysLysSerLeuThrAs 117  
|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
406 CAGTTGAGACCAAAACTGA.GTCAAGGGATTGCATAAGTCACTCACTGA 454

117 pValAlaLeuGluHisLysGluGluCysAspCysValCysArgGlySerT 134  
|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
455 TGTGGCTCTGGAACACCACAGGAGGATGTGACTGTGTGTAGAGGAACG 504

134 hrGlyGly 136  
:::|||||  
505 CAGGAGGG 512

seq\_name: gb\_est82:BF011835

seq\_documentation\_block:  
LOCUS BF011835 447 bp mRNA EST 06-OCT-2000  
DEFINITION us37d10.y1 Soares.NMEBA.branchial\_arch Mus musculus cDNA clone  
IMAGE:3169267 5' similar to TR:09Q71 Q9Q71 Q9Q71 FALLOTEIN. ;, mRNA  
sequence.

ACCESSION BF011835  
VERSION BF011835.1 GI:10712110  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 447)

AUTHORS: NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE: National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL: Unpublished (1997)  
COMMENT: Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo  
, Ph.D.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
image.llnl.gov/image/html/iresources.shtml

MGI:1064727  
Seq primer: -40RP from Gibco  
High quality sequence stop: 402.  
FEATURES  
Location/Qualifiers  
1..447  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="IMAGE:3169267"  
/clone\_lib="Soares.NMEBA.branchial\_arch"  
/tissue\_type="branchial arches"  
/dev\_stages="embryo, 10.5 dpc"  
/lab\_host="DH10B (phage resistant)"  
/note="Vector: pT73D-pac (Pharmacia) with a modified  
polylinker; Site\_1: NotI; Site\_2: EcoRI; 1st strand cDNA  
was primed with a Not I - oligo(dT) primer [5',  
TGTTACCAATCTGAAGTGGAGCGCCGATCTTTTTTTTTTTTTTTTTTTTT  
3']; Double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not  
I and Eco RI sites of the modified pT73 vector. Library  
constructed and normalized by Bento Soares and M.Fatima  
Bonaldo."

BASE COUNT 126 a 104 c 108 g 109 t  
ORIGIN

alignment\_scores:  
Quality: 587.00 Length: 116  
Ratio: 5.149 Gaps: 0  
Percent Similarity: 98.276 Percent Identity: 88.793

alignment\_block:  
US-09-457-066-2\_COPY\_210\_345 x BF011835 ..

Align seg 1/1 to: BF011835 from: 1 to: 447

1 LeuAspLeuGluAspLeuTyrArgProThrTrpGlnLeuLeuGlyLysAl 17  
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
100 GTGAGCTGGACAGCCTCTACAGCCACATGGCAGCTTTTGGCAAGGC 149

17 apheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThrG 34  
|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
150 TTTCTCTGTATGGGAAAAAAGCAAGTGGTGAATCTGAATCTCTCTCAAGG 199

34 luGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerIle 50  
|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
200 AAGAGGTAATAACTTACAGCTGCACACCCCGGAATCTCTCAGTGTCCATA 249

51 ArgGluGluLeuLysArgThrAspThrIlePheThrProGlyCysLeuLe 67  
|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
250 CGGAAGAGCTAAGAGAGACAGATACCATATCTTGGCCAGGTGTCTCTCT 299

67 uValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsnG 84  
|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
300 GGTCAAGCGCTGTGGAGGAAATTTGTGCTCTCTCCATAATTCGAATG 349

84 luCysGlnCysValProSerLysValThrLysLysTyrHisGluValLeu 100  
|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
350 AATGTCAGTGTGTCCCGAGGTAAGTTACAAAAAAGTACCATGAGGTCTCT 399

101 GlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 116  
 400 CAGTTGAGACCAAAAGCTGGAGTCAAGGGATTGCATAAATCACTACT 447

seq\_name: gb\_est28:AL047637

seq\_documentation\_block: 304 bp mRNA EST 01-MAR-2000  
 LOCUS AL047637  
 DEFINITION DKFZp586J0421\_r1 586 (synonym: hutel) Homo sapiens cDNA clone  
 DKFZp586J0421, mRNA sequence.  
 ACCESSION AL047637  
 VERSION AL047637.1 GI:4728633  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 304)  
 AUTHORS Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J., and  
 Wiemann, S.  
 TITLE EST (Ottenwaelder, et al.)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Ottenwaelder B  
 MIPS

Am Klopferspitz 18a D-82152 Martinsried, Germany  
 This is the 5' sequence of the clone insert  
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
 sequenced by MediGenomix\* (Martinsried/Germany) within the cDNA  
 sequencing consortium of the German Genome Project. No sl sequence  
 available.

This clone (DKFZp586J0421) is available at the RZPD in Berlin.  
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES  
 source

1..304  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="DKFZp586J0421"  
 /clone\_lib="586 (synonym: hutel)"  
 /tissue\_type="uterus"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /note="Vector: pSPORT1; Site\_1: NotI; Site\_2: SalI/MluI"  
 BASE COUNT 86 a 68 c 80 g 70 t

alignment\_scores:  
 Quality: 568.00 Length: 101  
 Ratio: 5.624 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 99.010

alignment\_block:  
 US-09-457-066-2\_COPY\_210\_345 x AL047637 ..

Align seg 1/1 to: AL047637 from: 1 to: 304

34 GluGluValArgLeuTyrSerCysThrProArgAspPheSerValSer11 50  
 2 GAGGAGGTAAGATTATACAGCTGCACACCTCGTAACCTTCTCAGTGTCCAT 51  
 50 eArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeuL 67  
 52 AAGGAGAGAACTAAAGACACCCATACCACTTTCTGGCCAGGTGTCTCC 101  
 67 euValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsn 83  
 102 TGGTTAAACGCTGTGTGGGAAGTGTGCTGTGTCTCCACATTCGAAT 151  
 84 GluCysGlnCysValProSerLysValThrLysLysLysLysLysValLe 100  
 152 GAATGTCAATGTGTCCCAAGCAAGTACTTAAAAAATACCACGAGGTCT 201

100 uGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 117  
 202 TCAGTTGAGACCAAAAGACCGGTGTCAAGGGATTGCACAAATCACTACCG 251  
 117 spValAlaLeuGluHisGluGluCysAspCysValCysArgGlySer 133  
 252 ACGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGC 301  
 134 Thr 134  
 ...  
 302 TCA 304

seq\_name: gb\_est91:BF670092

seq\_documentation\_block: 874 bp mRNA EST 21-DEC-2000  
 LOCUS BF670092  
 DEFINITION 602119417F1 NIH\_MGC\_56 Homo sapiens cDNA clone IMAGE:4276493 5',  
 mRNA sequence.  
 ACCESSION BF670092  
 VERSION BF670092.1 GI:11943987  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 874)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: CLONETECH Laboratories, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLC1097 row: a column: 06

High quality sequence stop: 598.

FEATURES  
 source

1..874  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4276493"  
 /clone\_lib="NIH\_MGC\_56"  
 /tissue\_type="primitive neuroectoderm"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /note="Organ: brain; Vector: pDNR-LIB (Clontech); Site\_1:  
 SfiI (ggcgctcgcc); Site\_2: SfiI (ggcattatggcc);  
 Double-stranded cDNA was prepared from cell line RNA. 5'  
 and 3' adaptors were used in cloning as follows: 5'  
 adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor  
 sequence: 5'-ATTCTAGAGCGGCGGCGGCGCATG-dT(30)BN-3',  
 (where B = A, C, G, or N = A, C, G, or T). Average  
 insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies  
 contained inserts by PCR. This library was enriched for  
 full-length clones and was constructed by Clontech  
 Laboratories (Palo Alto, CA)."  
 BASE COUNT 227 a 208 c 245 g 194 t  
 ORIGIN

alignment\_scores:  
 Quality: 538.50 Length: 143  
 Ratio: 4.240 Gaps: 10  
 Percent Similarity: 88.811 Percent Identity: 86.713

alignment\_block:  
 US-09-457-066-2\_COPY\_210\_345 x BF670092 ..

Align seg 1/1 to: BF670092 from: 1 to: 874

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1 LeuAspLeuGluAspLeuTyrArgProThrTrpGlnLeuLeuGlyLysAl 17
|||||
19 TTGGACTTAGAAGATCTATATAGCCAACTTGGCAACTTCTTGCAAGGC 68
|||||
17 aPheValPhe.GlyArgLysSerArgValValAspLeuAsnLeuLeuThr 33
|||||
69 TTGG...TTTGGGAAGAAATCCAGATGGTGATCTGGAACCTTCTAACA 115
|||||
34 GluGluValArgLeu..TyrSerCysThrProArgAsnPheSerValSer 49
|||||
116 GAGGAGTAAGATATATAGCATGTGTCACACCTCGTAACCTTCTCAGTGTCC 165
|||||
50 IleArg.GluGluLeuLysArgThrAspThrIle.PheTrpProGlyCys 65
|||||
166 ATAATGGGAAGAACTAAAGAGAACCGATACCATGTTCTTGCCAGGTTGT 215
|||||
66 LeuLeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCy 82
|||||
216 CTCCTGGTTAAACGCTGTGTGGGAACGTGCGCTGTGCTCCACAATG 265
|||||
82 sAsnGluCysGln.CysValProSerLysValThrLysLysTyrHis.Gl 98
|||||
266 CAATGAATGTCAAGTGTGTCACCAAGTACTAAAAATACCAAGCGA 315
|||||
98 uValLeuGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerL 115
|||||
316 GGTCCCTCAGTGTGAGACCAAGACCGGTGTGAGGATGGCACAATCAC 365
|||||
115 euThrAspValAlaLeuGluHis.HisGlu.GluCysAspCys.ValCys 130
|||||
366 TCACCCAGCGTGGCCCTGGAGCACCATGAGAGTGTGACTGGTGTGTGTC 415
|||||
131 ArgGlySerThr 134
|||||
416 AGAGGGAGGCACA 427
|||||
```

```
seq_name: gb_est82:BF031624
seq_documentation_block: 950 bp mRNA EST 10-OCT-2000
LOCUS BF031624
DEFINITION 601558104F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827760 5',
mRNA sequence.
ACCESSION BF031624
VERSION BF031624.1 GI:10739336
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 950)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM497 row: h column: 01
High quality sequence stop: 415.
Location/Qualifiers
1..950
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3827760"
/clone_lib="NIH_MGC_58"
/tissue_type="hypernephroma"
/lab_host="DH10B (T1 phage-resistant)"
```

```
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggcccctcgcc); Site_2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA.
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CAGGCGCATATGGC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGGAGCGGCGGACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.35 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
BASE COUNT 288 a 309 c 211 g 142 t
ORIGIN
alignment_scores:
Quality: 523.00 Length: 95
Ratio: 5.564 Gaps: 0
Percent Similarity: 98.947 Percent Identity: 97.895
alignment_block:
US-09-457-066-2_COPY_210_345 x BF031624
Align seg 1/1 to: BF031624 from: 1 to: 950
42 ThrProArgAsnPheSerValSerIleArgGluGluLeuLysArgThrAs 58
|||||
3 ACACCTCGTAACCTCTCAGTGTCTCAAGGAAGAACTAAAGAGAACCGA 52
|||||
58 pThrIlePheTrpProGlyCysLeuLeuValLysArgCysGlyGlyAsn 75
|||||
53 TACCATTCTTCTGGCCAGGTTGTCTCTCTGTTAAACGCTGTGGTGAAC 102
|||||
75 ysAlaCysCysLeuHisAsnCysAsnGluCysGlnCysValProSerLys 91
|||||
103 GTGCTGTCTCTCCACAATTCGAATGAATGTCATGTCACCAAGCAA 152
|||||
92 ValThrLysLysTyrHisGluValLeuGlnLeuArgProLysThrGlyVa 108
|||||
153 GTTACTAAAAATAFACCACGAGGTCTTCAGTTGAGACCAAGACCGGTGT 202
|||||
108 lArgGlyLeuHisLysSerLeuThrAspValAlaLeuGluHisHisGlu 125
|||||
203 CAGGGGATTGCACAAATCACTACCGACGTGGCCCTGGAGCACTATGAG 252
|||||
125 luCysAspCysValCysArgGlySerThrClyGly 136
|||||
253 AGTGTGACTGTGTGTGAGAGGAGGACAGGAGGA 287
|||||
seq_name: gb_est97:BG118707
seq_documentation_block: 968 bp mRNA EST 30-JAN-2001
LOCUS BG118707
DEFINITION 602348280F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4443498 5',
mRNA sequence.
ACCESSION BG118707
VERSION BG118707.1 GI:12612213
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 968)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
```



found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LAM10217 row: 0 column: 19

High quality sequence start: 8

High quality sequence stop: 574.

# FEATURES

Location/Qualifiers  
1. 968  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:443498"  
/clone\_lib="NIH\_MGC\_90"  
/tissue\_type="adenocarcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: liver; Vector: pCMV-SPORT6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally; oligo-dT primed.  
Average insert size 1.7 kb. Library enriched for  
full-length clones and constructed by Life Technologies.  
Note: this is a NIH\_MGC Library."

BASE COUNT 313 a 230 c 219 g 206 t  
ORIGIN

alignment\_scores:  
Quality: 507.00 Length: 136  
Ratio: 4.694 Gaps: 1  
Percent Similarity: 79.412 Percent Identity: 79.412

## alignment\_block:

US-09-457-066-2\_copy\_210\_345 x BG118707 ..

Align seg 1/1 to: BG118707 from: 1 to: 968

1 LeuAspLeuGluAspLeuTyrArgProThrGlnLeuLeuGlyLysAl 17  
174 TTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGC 222

17 aPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThrG 34

223 .TTTCTTTTGGAGAAATCCAGAGTGTGGATCTGAACCTTCTTAACAG 272

34 LuGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerIle 50

273 AGGA..... 276

51 ArgGluGluLeuLysArgThrAspThrIlePheThrProGlyCysLeuLe 67

277 .....GGTGTCTCCT 287

67 uValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsnG 84

288 GGTAAACGCTGTGTGGAACTGTGCTGTGTCTCCACAATTCGAATG 337

84 LuCysGlnCysValProSerLysValThrLysLysThrHisGluValLeu 100

338 AATGTCAATGTCTCCAGCAAGTTACTAAATAATACCAGAGGTCCTT 387

101 GlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThrAs 117

388 CAGTTGAGACCAAGACCGGTGTCTAGGGGATTGCACAAATCACTCACCGA 437

117 pValalaLeuGluHisHisGluGluCysAspCysValCysArgGlySerT 134

438 CGTGCC.CTGGAGACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCA 486

134 hrGlyGly 136

487 CAGGAGGA 494

seq\_name: gb\_gss3:CNS024MX

seq\_documentation\_block:

LOCUS CNS024MX 877 bp DNA GSS 12-MAY-2000

DEFINITION Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone

235A22 of library G from Tetraodon nigroviridis, genomic survey sequence.

AL180978 AL180978.1 GI:7819035

KEYWORDS GSS: genome survey sequence.

SOURCE Tetraodon nigroviridis.

# ORGANISM

Tetraodon nigroviridis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

1 (bases 1 to 877)

Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.

TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 877)

Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.

TITLE Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 877)

Genoscope.

TITLE Direct Submission

JOURNAL Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases

COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

## FEATURES

Source

1. .877

/organism="Tetraodon nigroviridis"

/db\_xref="taxon:99883"

/clone="235A22"

/clone\_lib="G"

/note="Genoscope sequence ID : COAG235BAL1SP1-end : PUC-Ori"

BASE COUNT 229 a 207 c 188 g 248 t 5 others

## ORIGIN

## alignment\_scores:

Quality: 439.50 Length: 270

Ratio: 3.632 Gaps: 4

Percent Similarity: 44.815 Percent Identity: 34.444

## alignment\_block:

US-09-457-066-2\_COPY\_210\_345 x CNS024MX/rev ..

Align seg 1/1 to reverse of: CNS024MX from: 1 to: 877

1 LeuAspLeuGluAspLeuTyrArgProThrGlnLeuLeuGlyLysAl 17

845 GTGGATATGGAGGAGTTGTACAACCATCTCGGATGTGCKGGGAAGTC 796

17 aPheValPheGlyArgLysSerArg.Val..... 26

795 ATTCATCCATAGTAAAAAAGCCAGAGGTAGGACATTTTCAGATGGACTCCC 746

26 ..... 26

745 GACAAGGAACCTATATGTTGGGGCAGAGTTTACAGAAAGKTCACACAC 696

27 .....ValAspLeu.AsnLeuLeuThr 33

695 CTTTCTCTTTATGCTCTTTTTCAGGAGGAGGAGATCTTTTAACTCTGCTGAGG 646

34 GluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerIle 50

:::|||||.....

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645 GATGAAGTGGGACTGTACAGCTGCACACCGGCAACTTCTCTGTCTTT 596
50 eArgGluLeuLeuLysArgThrAspThrIlePheTrpProGlyCysLeuL 67
595 GCGTGAGAGCTGAAGAGGACCGATGTAATTTCTCGCCAAAGCTGCTCC 546
67 euValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsn 83
545 TGGTGAATCGCTGGCGGAACATGCGGCTGCTCTCACCGCGTCTAC 496
84 GlysGlnCysValProSerLysValThrLysLysTyrHisGlu..... 98
495 GACTGCCAGTCGCTCCACCAAGGCTCAGGAAGAAATATCATGAGGTAA 446
98 ..... 98
445 TGCTAGCACTTCACTTGAGGATGATGTTTCCGTTTGGCTGCGCTTTAA 396
98 ..... 98
395 AAGATTTTGAATCGCGGTTTGAACCTTCACAAATTTTGTCTGTGCCAAT 346
98 ..... 98
345 ACACAATACTACAAATKCCAGACACTGTGAATGTACAAATACTTATCTGA 296
98 ..... 98
295 GCTTGAATAATTTGAGATCTGAGAGCAAAATCCACTTACACTGCAATATTG 246
98 ..... 98
245 TTTTAATACAAACAAATCAACAAATCAAGACCAAGCTAAATGCAATTT 196
98 ..... 98
195 GATCGAATAATGATCAGCTTATAGATGAATGTTGATGTCCACAAATG 146
99 .....ValLeuGlnLeuArgProLysThrGlyValArgGlyLeuHisL 113
145 TTGTCAGGTTCTGCTGCTGAAACATCGAAATGCTGGCAAGGCGTGCAGA 96
113 ysSerLeuThrAspValAlaLeuGluHisGluGluCysAspCysVal 129
95 AATCGTTGACCGAGCTGCCCTTAGAACACCAAGCAAGAAATGCGCTGCGTG 46
130 CysArg 131
45 TGTAAA 40
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seq\_name: gb\_est84:BF163629

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seq_documentation_block: 902 bp mRNA EST 30-OCT-2000
LOCUS BF163629 601769732F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3989215 5',
DEFINITION mRNA sequence.
ACCESSION BF163629
VERSION BF163629.1 GI:11044002
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 902)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-re@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
```

```
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9198 row: 0 column: 08
High quality sequence stop: 743.
FEATURES
    Location/Qualifiers
        1..902
            /organism="Mus musculus"
            /strain="C57BL/6J (f1)"
            /db_xref="taxon:10090"
            /clone="IMAGE:3989215"
            /clone_lib="NCI_CGAP_Lu29"
            /tissue_type="spontaneous tumor, metastatic to mammary.
            Stem cell origin."
            /lab_host="DH10B"
            /note="Organ: lung; Vector: pCMV-SPORT6; Site: 1: SalI;
            Site: 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
            Library constructed by Life Technologies. Investigator
            providing samples: Gilbert Smith, NIH"
        BASE COUNT 248 a 203 c 241 g 210 t
        ORIGIN

alignment_scores:
    Quality: 381.00 Length: 69
    Ratio: 5.603 Gaps: 0
    Percent Similarity: 98.551 Percent Identity: 92.754

alignment_block:
US-09-457-066-2_COPY_210_345 x BF163629 ..
Align seg 1/1 to: BF163629 from: 1 to: 902

68 ValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsnG1 84
||||:|||||
7 GTCGCGCTGTGGAGAAATGTGCTGTGCTCCATAATGCAATGA 56

84 uCysGlnCysValProSerLysValThrLysLysTyrHisGluValLeuG 101
|||||
57 ATCTCAGTGTGCCAGTAAAGTTACAAAAAGTACCATGAGTCTCTTC 106

101 InLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThrAsp 117
|||||
107 AGTTGACCAAAACCTGGAGTCAAGGATTCATAGTCACTCACTGAT 156

118 ValAlaLeuGluHisGluGluCysAspCysValCysArgGlySerTh 134
|||||
157 GTGGCTTGGACACCAAGCAAGTGTGCTGTGTAGAGAAACGC 206

134 rGlyGly 136
207 AGGAGG 213

seq_name: gb_hic:AK003359
seq_documentation_block: 1796 bp mRNA HTC 08-FEB-2001
LOCUS AK003359 18 days embryo cDNA, RIKEN full-length enriched
DEFINITION library, clone:1110003109, full insert sequence.
ACCESSION AK003359
VERSION AK003359.1 GI:12833975
KEYWORDS CAP trapper.
SOURCE Mus musculus (strain:C57BL/6J) 18 days embryo cDNA to mRNA,
clone:1110003109.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (sites)
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Methods Enzymol. 303, 19-44 (1999)
REFERENCE 2 (sites)
```

**AUTHORS** Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

**TITLE** Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

**JOURNAL** Genome Res. 10 (10), 1617-1630 (2000)

**MEDLINE** 20499374

3 (sites)  
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
Koono, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M.,  
Kikuchi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T.,  
Harada, A., Yamamoto, R., Nakumoto, H., Sakaguchi, S., Ikegami, T.,  
Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,  
Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,  
Matsura, S., Okazaki, Y., Muramatsu, M., Inoue, Y. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system—384-format  
sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
20530913

REFERENCE 4 (sites)

**THE RIKEN GENOME EXPLORATION RESEARCH GROUP PHASE II TEAM AND FANTOM CONSORTIUM.**

## COMMENT

Contact: Marra M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of MedicineP  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:898546  
Seq primer: -28ml3 rev2 ET from Amersham  
High quality sequence stop: 283.

## FEATURES

## source

## Location/Qualifiers

1..324  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1365326"  
/clone\_lib="Soares\_mammary\_gland\_NbMMG"  
/sex="male"  
/tissue\_type="mammary gland"  
/dev\_stage="4 weeks"  
/lab\_host="DH10B"  
/note="Organ: mammary gland; Vector: pMT3D-Pac (Pharmacia  
) with a modified polylinker; Site\_1: Not I; Site\_2: Eco  
RI; 1st strand cDNA was primed with a Not I - oligo(dT)  
primer (5'  
TGTTACCAATCTGAATGGGAGCGCGGAATGGTTTTTTTTTTTTTTTTTT  
T 3'); double-stranded cDNA was ligated to Eco RI  
adaptors (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of the modified pMT3 vector.  
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library  
constructed and normalized by Bento Soares and M.Fatima  
Bonaldo."

BASE COUNT 82 a 81 c 81 g 80 t

## ORIGIN

## alignment\_scores:

Quality: 327.00 Length: 71  
Ratio: 4.739 Gaps: 0  
Percent Similarity: 97.183 Percent Identity: 83.099

## alignment\_block:

US-09-457-066-2\_COPY\_210\_345 x AI020581 ..

Align seg 1/1 to: AI020581 from: 1 to: 324

1 LeuAspLeuGluAspLeuTyrArgProThrTrpGlnLeuLeuGlyLysAl 17  
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
112 GTGGACTTGGACAGCCTCTACAGCCAAACATGGCAGCTTTGGGCAAGGC 161  
17 apheValPheGlyArgLysSerArgValValAspLeuAsnLeuThrG 34  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
162 TTTCTCTGTATGTGAAAAAAGCAAGTGGTGAATCTGAATCTCCTCAAGG 211  
34 iuGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerIle 50  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
212 AAGAGGTAAACTCTACAGCTGCACACCCCGGAACTTCTCAGTGTCCATA 261  
51 ArgGluGluLeuLysArgThrAspThrIlePheThrProGlyCysLeuLe 67  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
262 CGGAAGAGCTAAGAGGACAGATACCATATTCTGGCCAGGTTGTCTCCT 311  
67 uValLysArgCys 71  
|||||:|||||  
312 GGTCAAGCGCTGT 324

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 18, 2001, 01:12:39 ; Search time 50.8 Seconds

(without alignments)

162.300 Million cell updates/sec

Title: US-09-457-066-2\_COPY\_210\_345

Perfect score: 754

Sequence: 1 LDLELDYPTWQLLKAFV.....DVALEHHECDVCRGSTGG 136

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_0601.\*  
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.\*  
8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.\*  
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11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
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21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results, predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	754	100.0	318	21	AA1984558
2	754	100.0	339	21	AA1984558
3	754	100.0	345	20	AA1984558
4	754	100.0	345	20	AA1984558
5	754	100.0	345	20	AA1984558
6	754	100.0	345	21	AA1984558
7	754	100.0	345	21	AA1984558
8	754	100.0	345	21	AA1984558
9	754	100.0	345	21	AA1984558
10	754	100.0	345	21	AA1984558
11	754	100.0	345	21	AA1984558

12	754	100.0	345	21	AA1984558
13	754	100.0	345	21	AA1984558
14	754	100.0	345	21	AA1984558
15	754	100.0	345	21	AA1984558
16	754	100.0	345	21	AA1984558
17	754	100.0	345	21	AA1984558
18	754	100.0	345	21	AA1984558
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23	754	100.0	345	21	AA1984558
24	754	100.0	345	21	AA1984558
25	754	100.0	345	21	AA1984558
26	754	100.0	345	21	AA1984558
27	754	100.0	345	21	AA1984558
28	754	100.0	345	21	AA1984558
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30	754	100.0	345	21	AA1984558
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32	754	100.0	345	21	AA1984558
33	754	100.0	345	21	AA1984558
34	754	100.0	345	21	AA1984558
35	754	100.0	345	21	AA1984558
36	754	100.0	345	21	AA1984558
37	754	100.0	345	21	AA1984558
38	754	100.0	345	21	AA1984558
39	754	100.0	345	21	AA1984558
40	754	100.0	345	21	AA1984558
41	754	100.0	345	21	AA1984558
42	754	100.0	345	21	AA1984558
43	754	100.0	345	21	AA1984558
44	754	100.0	345	21	AA1984558
45	754	100.0	345	21	AA1984558

#### ALIGNMENTS

RESULT 1

AA1984558  
ID AA1984558 standard; Protein; 318 AA.

AC AA1984558;

DT 25-JUL-2000 (first entry)

XX A fragment of platelet-derived growth factor C (PDGF-C).

DE Platelet-derived growth factor C; PDGF-C; cell proliferation;  
growth factor; heparin; connective tissue; wound healing; VEGF-E;  
fibroblast mitogenesis; PDGF alpha receptor activation; tumour growth;  
chondrocarcinoma; Wilms tumour; megakaryoblastic leukaemia;  
lung carcinoma; erythroleukemia; tissue remodelling.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 287 /note= "encoded by AAS"

XX WO200018212-A2.

XX 06-APR-2000.

XX 30-SEP-1999; 99WO-US22668.

XX 30-SEP-1998; 98US-0102461.

XX 12-NOV-1998; 98US-0108109.

XX 03-DEC-1998; 98US-0110749.

XX 18-DEC-1998; 98US-0113002.

XX 21-MAY-1999; 99US-0135426.

XX 15-JUL-1999; 99US-0144022.

Human VEGF-X prote  
Human VEGF-X prote  
Human 990126veg p  
Human VEGF-X prote  
Human VEGF-X prote  
Human PRO200 (vasc  
Human PRO200 prote  
Human PRO713 prote  
Human TANGO 128.  
Human growth facto  
Human growth facto  
Amino acid sequenc  
Bone morphogenic p  
Human PRO200 prote  
Human PRO200 prote  
Human anglogenesis  
Human VEGF-X prote  
Human VEGF-X prote  
Human VEGF-X prote  
Human VEGF-X prote  
Mouse zvegf3, SEQ  
Murine vascular en  
A murine platelet-  
Human VEGF-X PDGF-  
Human VEGF-X prote  
Human VEGF-X prote  
Human VEGF-X prote  
Human VEGF-X prote  
Mouse growth facto  
Human Platelet Der  
Human growth facto  
SEQ. ID. 37 from W  
Human Platelet Der  
Human VEGF-G prote  
Human VEGF-G prote

XX (LUDW-) LUDWIG INST CANCER RES.  
PA (UYHE-) UNIV HELSINKI LICENSING LTD.  
XX Eriksson U, Aase K, Lee X, Ponten A, Dutela M, Alitalo K;  
PI Oestman A, Heldin C, Betsholz C;  
XX WPI; 2000-292954/25.  
XX N-PSDB; AAA12524.  
XX Novel DNA encoding PDGF-C useful to stimulate or enhance proliferation,  
PT differentiation, growth and motility of cells expressing the PDGF-C  
PT receptor  
XX  
XX Disclosure; Fig 4; 135pp; English.  
XX  
XX The present sequence represents a human platelet-derived growth factor C  
CC (PDGF-C) (formally designated VEGF-F) fragment. PDGF-C polypeptides have  
CC the ability to stimulate and enhance proliferation or differentiation,  
CC and/or growth or motility of cells expressing a PDGF-C receptor.  
CC PDGF-C polypeptides can be used in pharmaceuticals for promoting cell  
CC proliferation, preferably in combination with one other growth factor  
CC and heparin. Pharmaceuticals comprising PDGF-C polypeptides can also  
CC be used for stimulating connective tissue or wound healing. The  
CC PDGF-C polypeptide can be enzymatically processed to generate the active  
CC truncated form of PDGF-C and used to regulate the receptor-binding  
CC specificity of PDGF-C. PDGF-C can also be used to promote fibroblast  
CC mitogenesis in a mammal and to induce PDGF alpha receptor activation.  
CC PDGF-C antagonists can be used to inhibit tumour growth of a tumour  
CC expressing PDGF-C in a mammal. Specific types of human tumours, e.g.  
CC choriocarcinoma, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma  
CC and erythroleukemia, can be identified by testing for expression of  
CC PDGF-C. PDGF-C antagonists can also be used to inhibit tissue  
CC remodelling during invasion of tumour cells into a normal population of  
CC cells. Antagonists can also be used to treat fibrotic conditions,  
CC especially found in the lung, kidney or liver.  
XX  
XX Sequence 318 AA;  
SQ

Query Match 100.0%; Score 754; DB 21; Length 318;  
Best Local Similarity 100.0%; Pred. No. 4.3e-71;  
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDLEDLYRPTWQLLGKAFVFGKRSRVVDNLNLTTEEVRLYSCTPRNFSVSIREELKRTDTI 60  
Db 183 LDLEDLYRPTWQLLGKAFVFGKRSRVVDNLNLTTEEVRLYSCTPRNFSVSIREELKRTDTI 242  
Qy 61 FWPGCLLVKRCGGNCACCLHNCNECQVPSKVTYKHYEVLQRLPKTGVRLHKSILTDVAL 120  
Db 243 FWPGCLLVKRCGGNCACCLHNCNECQVPSKVTYKHYEVLQRLPKTGVRLHKSILTDVAL 302  
Qy 121 EHHEECDCVCRGSTGG 136  
Db 303 EHHEECDCVCRGSTGG 318

RESULT 2  
AAB58438  
ID AAB58438 standard; Protein; 339 AA.  
XX  
XX AAB58438;  
XX  
XX 14-MAR-2001 (first entry)  
XX  
XX Lung cancer associated polypeptide sequence SEQ ID 776.  
XX  
XX Human; lung cancer associated protein; neuroprotective; cytoskeletal;  
XX cardioactive; immunomodulatory; muscular active; vulnarary;  
XX gastrointestinal; nephrotropic; antiinfective; gynecological;  
XX antibacterial; diagnosis; neural disorder; immune disorder; reproductive;  
XX proliferative disorder; wound healing; infectious disease.  
XX

OS Homo sapiens.  
XX  
XX WO200055180-A2.  
XX  
XX 21-SEP-2000.  
XX  
XX 08-MAR-2000; 2000WO-US05918.  
XX  
XX 12-MAR-1999; 99US-0124270.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA (ROSE/) ROSEN C A.  
XX  
XX Ruben SM;  
PI  
XX  
XX WPI; 2000-587514/55.  
DR N-PSDB; AAF18314.  
DR  
XX  
XX Lung cancer associated gene sequences, referred to as lung cancer  
PT antigens, useful for treatment, prevention, and diagnosis of disorders  
PT such as lung cancer  
XX  
XX Claim 11; Page 1305-1306; 1425pp; English.  
XX  
XX Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer  
CC associated proteins represented in AAB58106 - AAB58548. Lung cancer  
CC associated proteins and polynucleotide sequences, their agonists, and  
CC antagonists may have neuroprotective; cytostatic; cardioactive;  
CC immunomodulatory; muscular active general; vulnarary; gastrointestinal  
CC general; nephrotropic; antiinfective; gynecological; or antibacterial  
CC activity. The invention also includes antibodies specific for the  
CC protein or polynucleotide sequences. The lung cancer associated  
CC polynucleotide sequences may be used for detection of lung cancer,  
CC chromosome identification, as chromosome markers, and for numerous other  
CC diagnostic or research purposes. The proteins may be used to treat  
CC disorders such as neural, immune, muscular, reproductive,  
CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative  
CC disorders. The proteins may also be used in the treatment of wounds and  
CC infectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and  
CC peptide AAB58549 are used in the course of the invention for the  
CC identification and characterisation of the polynucleotide and protein  
CC sequences.  
XX  
XX Sequence 339 AA;  
SQ

Query Match 100.0%; Score 754; DB 21; Length 339;  
Best Local Similarity 100.0%; Pred. No. 4.6e-71;  
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDLEDLYRPTWQLLGKAFVFGKRSRVVDNLNLTTEEVRLYSCTPRNFSVSIREELKRTDTI 60  
Db 204 LDLEDLYRPTWQLLGKAFVFGKRSRVVDNLNLTTEEVRLYSCTPRNFSVSIREELKRTDTI 263  
Qy 61 FWPGCLLVKRCGGNCACCLHNCNECQVPSKVTYKHYEVLQRLPKTGVRLHKSILTDVAL 120  
Db 264 FWPGCLLVKRCGGNCACCLHNCNECQVPSKVTYKHYEVLQRLPKTGVRLHKSILTDVAL 323  
Qy 121 EHHEECDCVCRGSTGG 136  
Db 324 EHHEECDCVCRGSTGG 339

RESULT 3  
AAY33679  
ID AAY33679 standard; Protein; 345 AA.  
XX  
XX AAY33679;  
XX  
XX 11-JAN-2000 (first entry)  
XX  
XX Human VEGF-E protein.  
XX

KW VEGF-E; human; vascular endothelial cell growth factor; wound repair;  
 KW treatment; cardiovascular disorder; endothelial disorder; therapy;  
 KW tissue generation; regeneration; cardiac hypertrophy; cancer; detection;  
 KW angiogenic disorder; age-related macular degeneration; vascular disease;  
 KW neovascularization; tumor; gene mapping.

XX Homo sapiens.

XX WO9947677-A2.

XX 23-SEP-1999.

XX 10-MAR-1999; 99WO-US05190.

XX 17-MAR-1998; 98US-0040220.

XX 02-NOV-1998; 98US-0184216.

XX (GETH ) GENENTECH INC.

XX Ferrara N, Kuo SS;

XX WPI; 1999-580306/49.

XX N-PSDB; AAZ23691.

XX New growth factor polypeptide useful for treating cardiovascular or  
 PT endothelial disorders, e.g. cardiac hypertrophy

XX Claim 1; Fig 2; 122pp; English.

XX This invention describes the isolation of a novel human vascular  
 CC endothelial cell growth factor-E (VEGF-E) polypeptide which has  
 CC tranquilizer, vulnery and cardiant activity. VEGF-E can be administered  
 CC therapeutically, especially by expressing encoding polynucleotides, to  
 CC treat cardiovascular or endothelial disorders in mammals, especially  
 CC humans. It is useful in wound repair and tissue generation and  
 CC regeneration, and may especially be used to treat cardiac hypertrophy  
 CC It can be combined with a carrier in pharmaceutical compositions, which  
 CC can be administered to treat disorders as above. VEGF-E can be used to  
 CC screen for antagonists and agonists, and the antagonists administered to  
 CC treat angiogenic disorders in mammals (especially humans) e.g. cancer or  
 CC age-related macular degeneration. It can be used to generate antibodies,  
 CC useful therapeutically as antagonists, as above. The antibodies are also  
 CC useful to detect VEGF-E polypeptide, especially to diagnose  
 CC cardiovascular, endothelial or angiogenic disorders in mammals (e.g.  
 CC vascular disease, or neovascularization associated with tumor formation),  
 CC by contacting the antibody with a tissue sample and detecting formation  
 CC of an antibody-VEGF-E polypeptide complex. Polynucleotides encoding  
 CC VEGF-E can be used to diagnose cardiovascular and endothelial disorders  
 CC in mammals, by detecting abnormally high or low VEGF-E gene expression in  
 CC tissue samples. They can also be used to diagnose a disease or  
 CC susceptibility to a disease related to a mutated form of VEGF-E (e.g. a  
 CC cardiovascular, endothelial or angiogenic disorder such as a tumor), by  
 CC detecting a mutation in the VEGF-E-encoding sequence isolated from a  
 CC sample. They may also be used to produce probes useful to detect related  
 CC sequences or for gene mapping. This sequence represents the human VEGF-E  
 CC protein described in the method of the invention.

XX Sequence 345 AA;

Query Match 100.0%; Score 754; DB 20; Length 345;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-71;  
 Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDLEDLYPTWQLGKARVFGKSRVDNLNLTTEVRVLSYCTPRNFSVIRELKTDTI 60

DB 210 ldledlyptwqlgkatvfgkrsrvdnlnteervlyscyprnfsvireelkrttdi 269

QY 61 FWPGLLVKRCGGNCACCLHNCNCCQVPSKVKYHYEVLQLRPKTGVRGLHSLTDLVAL 120

DB 270 fwpgccllvkrcggncacclhncnccqvpksvkkyhevlqlrptgtvrglnksltdval 329

QY 121 EHHEECDCVCRSTGG 136

Db 330 ehheecdcvcrstgg 345  
 RESULT 4  
 AAY41766  
 ID AAY41766 standard; Protein; 345 AA.  
 XX  
 AC AAY41766;  
 XX  
 DT 07-DEC-1999 (first entry)  
 XX  
 DE Human PRO200 protein sequence.  
 XX  
 KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;  
 KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;  
 KW secreted protein; transmembrane protein.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9946281-A2.  
 XX  
 PD 16-SEP-1999.  
 XX  
 PF 08-MAR-1999; 99WO-US05028.  
 XX  
 PR 10-MAR-1998; 98US-0077450.  
 PR 11-MAR-1998; 98US-0077632.  
 PR 11-MAR-1998; 98US-0077641.  
 PR 11-MAR-1998; 98US-0077649.  
 PR 12-MAR-1998; 98US-0077791.  
 PR 13-MAR-1998; 98US-0078004.  
 PR 17-MAR-1998; 98US-0040220.  
 PR 20-MAR-1998; 98US-0078886.  
 PR 20-MAR-1998; 98US-0078910.  
 PR 20-MAR-1998; 98US-0078936.  
 PR 20-MAR-1998; 98US-0078939.  
 PR 25-MAR-1998; 98US-0079294.  
 PR 26-MAR-1998; 98US-0079656.  
 PR 27-MAR-1998; 98US-0079663.  
 PR 27-MAR-1998; 98US-0079664.  
 PR 27-MAR-1998; 98US-0079689.  
 PR 27-MAR-1998; 98US-0079728.  
 PR 27-MAR-1998; 98US-0079786.  
 PR 30-MAR-1998; 98US-0079920.  
 PR 30-MAR-1998; 98US-0079923.  
 PR 31-MAR-1998; 98US-0080105.  
 PR 31-MAR-1998; 98US-0080107.  
 PR 31-MAR-1998; 98US-0080165.  
 PR 31-MAR-1998; 98US-0080194.  
 PR 01-APR-1998; 98US-0080327.  
 PR 01-APR-1998; 98US-0080328.  
 PR 01-APR-1998; 98US-0080333.  
 PR 01-APR-1998; 98US-0080334.  
 PR 08-APR-1998; 98US-0081049.  
 PR 08-APR-1998; 98US-0081070.  
 PR 08-APR-1998; 98US-0081071.  
 PR 09-APR-1998; 98US-0081195.  
 PR 09-APR-1998; 98US-0081203.  
 PR 09-APR-1998; 98US-0081229.  
 PR 15-APR-1998; 98US-0081817.  
 PR 15-APR-1998; 98US-0081838.  
 PR 15-APR-1998; 98US-0081952.  
 PR 15-APR-1998; 98US-0081955.  
 PR 21-APR-1998; 98US-0082568.  
 PR 21-APR-1998; 98US-0082569.  
 PR 22-APR-1998; 98US-0082700.  
 PR 22-APR-1998; 98US-0082704.  
 PR 22-APR-1998; 98US-0082804.  
 PR 23-APR-1998; 98US-0082767.  
 PR 23-APR-1998; 98US-0082796.  
 PR 27-APR-1998; 98US-0083336.  
 PR 28-APR-1998; 98US-0083322.

PR 29-APR-1998; 98US-0083392.  
 PR 29-APR-1998; 98US-0083495.  
 PR 29-APR-1998; 98US-0083496.  
 PR 29-APR-1998; 98US-0083499.  
 PR 29-APR-1998; 98US-0083500.  
 PR 29-APR-1998; 98US-0083545.  
 PR 29-APR-1998; 98US-0083554.  
 PR 29-APR-1998; 98US-0083558.  
 PR 29-APR-1998; 98US-0083559.  
 PR 30-APR-1998; 98US-0083742.  
 PR 05-MAY-1998; 98US-0084366.  
 PR 06-MAY-1998; 98US-0084414.  
 PR 06-MAY-1998; 98US-0084441.  
 PR 07-MAY-1998; 98US-0084598.  
 PR 07-MAY-1998; 98US-0084600.  
 PR 07-MAY-1998; 98US-0084627.  
 PR 07-MAY-1998; 98US-0084637.  
 PR 07-MAY-1998; 98US-0084639.  
 PR 07-MAY-1998; 98US-0084640.  
 PR 07-MAY-1998; 98US-0084643.  
 PR 13-MAY-1998; 98US-0085323.  
 PR 13-MAY-1998; 98US-0085338.  
 PR 13-MAY-1998; 98US-0085339.  
 PR 15-MAY-1998; 98US-0085573.  
 PR 15-MAY-1998; 98US-0085579.  
 PR 15-MAY-1998; 98US-0085580.  
 PR 15-MAY-1998; 98US-0085582.  
 PR 15-MAY-1998; 98US-0085689.  
 PR 15-MAY-1998; 98US-0085697.  
 PR 15-MAY-1998; 98US-0085700.  
 PR 15-MAY-1998; 98US-0085704.  
 PR 18-MAY-1998; 98US-0086023.  
 PR 22-MAY-1998; 98US-0086392.  
 PR 22-MAY-1998; 98US-0086414.  
 PR 22-MAY-1998; 98US-0086430.  
 PR 22-MAY-1998; 98US-0086486.  
 PR 28-MAY-1998; 98US-0087098.  
 PR 28-MAY-1998; 98US-0087106.  
 PR 28-MAY-1998; 98US-0087208.  
 PR 30-JUL-1998; 98US-0094651.  
 PR 11-SEP-1998; 98US-0100038.  
 XX (GETH ) GENENTECH INC.

PA (GETH ) GENENTECH INC.

XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;

XX WPI; 1999-551358/46.

DR N-PSDB; AAZ34296.

XX New secreted and transmembrane polypeptides and their polynucleotides,  
 PT useful for treating blood coagulation disorders, cancers and cellular  
 PT adhesion disorders

XX Claim 12; Fig 207; 530pp; English.

XX The present invention describes secreted and transmembrane polypeptides  
 CC and their polynucleotides. The nucleotide sequences are useful as  
 CC sources of probes, primers, for chromosome mapping, and for generation  
 CC of antisense sequences. They can also be used to create transgenic  
 CC animals. The proteins can be used to treat a variety of diseases and  
 CC disorders, depending on their function. Diseases that may be treated  
 CC include blood coagulation disorders, cancers and cellular adhesion  
 CC disorders. They may also be used to raise antibodies. AAZ33891 to  
 CC AAZ34338, and AA41685 to AA41774 represent polynucleotide and  
 CC polypeptide sequence given in the exemplification of the present  
 CC invention.

XX Sequence 345 AA;

Query Match 100.0%; Score 754; DB 20; Length 345;

Best Local Similarity 100.0%; Pred. No. 4.7e-71;

Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDLEDLYRPTWQLLGKAFVFGKRSRVVDNLLTEVRLYSCTPRNFSVSIREELKRTDTI 60  
 .  
 Db 210 ldledlyrptwqllgkafvfgkrsvvdnlilteevrlyscprnfsvsireelkrtdti 269  
 |||||  
 Qy 61 FWPGCLLVKRCGNCACCLHNCNCCVPSKVTKYHEVLQLRPKTVGRGLHKLTDVAL 120  
 |||||  
 Db 270 fwpgccllvkrcgncacclhncnccvpskvtkyhevlglrpkgtvgrghksltldval 329  
 |||||  
 Qy 121 EHHBECDCVCRGSTGG 136  
 |||||  
 Db 330 ehheecdvcrgstgg 345  
 |||||

RESULT 5

AAV30023

ID AAV30023 standard; Protein; 345 AA.

XX AAV30023;

AC AAV30023;

XX 11-OCT-1999 (first entry)

XX Human vascular endothelial growth factor related protein.

DE Vascular endothelial growth factor related protein; VEGF-R protein;  
 KW tissue growth inhibition; tumour growth; cancer; tissue growth;  
 KW angiogenesis; coronary artery blockage.

XX Homo sapiens.

XX WO9937671-A1.

XX 29-JUL-1999.

XX 26-JAN-1999; 99WO-US01574.

XX 31-AUG-1998; 98US-0098548.

XX 27-JUN-1998; 98US-0072635.

XX 05-JUN-1998; 98US-0088089.

XX 24-JUN-1998; 98US-0090544.

XX (ELIL ) LILLY & CO ELI.

XX Dou S, Na S, Song HY;

XX WPI; 1999-458680/38.

DR N-PSDB; AA86352.

XX A vascular endothelial growth factor related protein and related  
 PT polynucleotide, useful for identifying antagonists and binding  
 PT compounds

XX Claim 1; Page 56-58; 62pp; English.

XX The present sequence represents a vascular endothelial growth factor  
 CC related (VEGF-R) protein. VEGF-R can be used in assays to identify  
 CC compounds that bind to it or that antagonize its activity. VEGF-R  
 CC antagonists (e.g. anti-VEGF-R antibodies) are useful for inhibiting  
 CC tissue growth. This is useful for inhibiting tumour growth and for  
 CC treating cancer. VEGF-R itself can be used to stimulate tissue  
 CC growth, angiogenesis and to treat coronary artery blockage. The  
 CC VEGF-R coding sequence can be used for the recombinant production of  
 CC the VEGF-R protein.

XX Sequence 345 AA;

XX Query Match 100.0%; Score 754; DB 20; Length 345;

Best Local Similarity 100.0%; Pred. No. 4.7e-71;

Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDLEDLYRPTWQLLGKAFVFGKRSRVVDNLLTEVRLYSCTPRNFSVSIREELKRTDTI 60  
 |||||



Db 210 ldledlyrptwllgkafvgrksrvvdlntlteevrlyscptprnfsvsireelkrtdti 269  
 QY 61 FWPGCLLVKRCGNCACCLHNCQCVPKSKVTKYHEVLQRLPKTGVRGLHKSITDVAL 120  
 Db 270 fwpqcllvkrcgncacclhncqcvpakvtkkyhevlqlrpkgtgvrghksitdval 329  
 QY 121 EHHEEDCVCRCSTGG 136  
 Db 330 ehheecdvcrcgstg 345

RESULT 6  
 AAB48657  
 ID AAB48657 standard; Protein; 345 AA.  
 AC AAB48657;  
 XX  
 DT 09-MAR-2001 (first entry)  
 XX  
 DE Human zvegf3, SEQ ID NO:33.  
 XX  
 KW Human; zvegf3; zvegf4 fusion; growth factor homologue; VEGF/PDGF family;  
 KW CUB domain; PDGF-like activity; mitogenic; osteogenic;  
 KW neovascularisation; tissue repair; proliferation; differentiation;  
 KW liver damage; neurodegenerative; Alzheimer's disease; multiple sclerosis;  
 KW periodontal disease; bone fracture; wound healing; vulnery; ischaemia;  
 KW immunomodulation; hepatic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200066736-A1.  
 XX  
 PD 09-NOV-2000.  
 XX  
 PF 03-MAY-2000; 2000WO-US40047.  
 XX  
 PR 03-MAY-1999; 99US-0304216.  
 PR 10-NOV-1999; 99US-0164463.  
 PR 04-FEB-2000; 2000US-0180169.  
 XX  
 PA (ZYMO ) ZYMOGENETICS INC.  
 XX  
 PI Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;  
 WPI; 2000-687541/67.  
 N-PSDB; AAC81582.  
 XX  
 PT Growth factor homologs and the nucleic acids that encode them, useful  
 e.g. for treating liver damage, ischemia, multiple sclerosis and  
 PT Alzheimer's disease -  
 XX  
 PS Claim 48; Page 125-126; 143pp; English.  
 XX  
 CC The invention relates to the human growth factor homologue zvegf4  
 CC (AAB48653), and nucleic acids encoding it (AAC81555). Zvegf4 is a member  
 CC of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial  
 CC growth factor) family. Zvegf4 has a growth factor domain (AAB48654)  
 CC characterised by a PDGF cystine knot structure, and a CUB domain  
 CC (AAB48655) which has a beta barrel structure. Zvegf4 has PDGF-like  
 CC activity, having mitogenic activity on fibroblasts, vascular smooth  
 CC muscle cells and pericytes, and has also been shown to stimulate bone  
 CC growth. The invention also relates to fusion proteins comprising human  
 CC zvegf4 or fragments thereof, particularly human zvegf4/human zvegf3  
 CC fusions; expression constructs and host cells comprising human zvegf4  
 CC nucleic acids; the recombinant expression of human zvegf4; an antibody  
 CC which binds to human zvegf4 or a fragment thereof; a method of activating  
 CC a cell-surface PDGF receptor using a zvegf4-derived polypeptide; a  
 CC method of modulating the proliferation, differentiation, migration or  
 CC metabolism of bone cells, comprising exposing bone cells to  
 CC zvegf4-derived polypeptides; and a method of detecting a genetic  
 CC abnormality in the zvegf4 gene of a patient. Zvegf4 proteins and derived  
 CC fragments may be used to stimulate tissue development or repair, or  
 CC cellular differentiation or proliferation. They are particularly used for

CC the treatment or repair of liver damage, and may also be used to  
 CC modulate neurite growth (e.g., in the treatment of Alzheimer's disease or  
 CC multiple sclerosis). Due to their osteogenic activity, they may be used  
 CC in the treatment of periodontal disease and fractures. They may also be  
 CC used to enhance expansion and mobilisation of haematopoietic stem cells  
 CC and endothelial precursor stem cells, which may be useful in the  
 CC treatment of ischaemia, in wound healing, and in the modulation of the  
 CC immune system. The present sequence represents human zvegf3.  
 XX  
 SQ Sequence 345 AA;  
 Query Match 100.0%; Score 754; DB 21; Length 345;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-71;  
 Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDLEDLYRPTWOLLGKAFVGRKSRVVVDLNTLLEEVRLYSCTPRNFSVSIREELKRDTDTI 60  
 Db 210 ldledlyrptwllgkafvgrksrvvdlntlteevrlyscptprnfsvsireelkrtdti 269  
 QY 61 FWPGCLLVKRCGNCACCLHNCQCVPKSKVTKYHEVLQRLPKTGVRGLHKSITDVAL 120  
 Db 270 fwpqcllvkrcgncacclhncqcvpakvtkkyhevlqlrpkgtgvrghksitdval 329  
 QY 121 EHHEEDCVCRCSTGG 136  
 Db 330 ehheecdvcrcgstg 345

RESULT 7  
 AAB24250  
 ID AAB24250 standard; Protein; 345 AA.  
 XX  
 AC AAB24250;  
 XX  
 DT 08-FEB-2001 (first entry)  
 XX  
 DE Human platelet-derived growth factor related protein LP8.  
 XX  
 KW Human; platelet derived growth factor related protein; LP8; VEGFh;  
 KW vascular endothelial growth factor h; tissue regeneration; vulnery;  
 KW atherosclerosis; PDGF-related protein; antiarteriosclerotic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200059940-A2.  
 XX  
 PD 12-OCT-2000.  
 XX  
 PF 24-MAR-2000; 2000WO-US06427.  
 XX  
 PR 06-APR-1999; 99US-0127913.  
 XX  
 PA (ELIL ) LILLY & CO ELI.  
 XX  
 PI Hammond LJ, Na S;  
 XX  
 DR WPI; 2000-664991/64.  
 DR N-PSDB; AAC64426.  
 XX  
 PT Enhancing tissue growth and promoting wound healing by administering  
 platelet-derived growth factor related protein, LP8 or its analog and  
 PT treating atherosclerosis by administering LP8 antagonist -  
 XX  
 PS Claim 4; Page 63-64; 64pp; English.  
 XX  
 CC The present invention describes a method for enhancing tissue growth,  
 CC promoting wound healing or stimulating smooth muscle growth by  
 CC administering a platelet-derived growth factor (PDGF) related protein,  
 CC designated LP8 or its analogue. Also described is a method of slowing  
 CC the progress of atherosclerosis or treating atherosclerosis comprising  
 CC the administration of an LP8 antagonist. The method is useful for  
 CC enhancing tissue growth, promoting wound healing and stimulating smooth

CC muscle growth. Antagonists of LP8 are useful for treating  
 CC atherosclerosis. The present sequence represents human LP8, which is  
 CC also called VEGFh.  
 XX  
 XX  
 SQ Sequence 345 AA;

Query Match 100.0%; Score 754; DB 21; Length 345;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-71;  
 Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDLEDLYRPTWQLGKAFVGRKSRVVDNLNLTTEVRLYSCTPRNFSVSIREELKRTDTI 60  
 Db 210 ldledlyrptwqlgkafvgrksrvvdnlnteervrlyscprnfsvsireelkrtdti 269  
 QY 61 FWPGGCLLVKRCGNCACCLHNCQCVPKSKYTKYHEVLQRLPKTGVRLHKLSTLTDVAL 120  
 Db 270 fwpgcllvkrcgncacclhncqcvpkskkyhevlqlrpkgtgvrghklsldval 329  
 QY 121 EHHEECDCVCRGSGTG 136  
 Db 330 ehheecdvcrgstgg 345

RESULT 8  
 AAB44322  
 ID AAB44322 standard; Protein; 345 AA.  
 XX  
 AC AAB44322;  
 XX  
 DT 08-FEB-2001 (first entry)  
 XX  
 DE Human PRO200 (UNQ174) protein sequence SEQ ID NO:488.  
 XX  
 KW Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;  
 KW expressed sequence tag; detection; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200053756-A2.  
 XX  
 PD 14-SEP-2000.

XX 18-FEB-2000; 2000WO-US04341.  
 XX  
 XX 08-MAR-1999; 99WO-US05028.  
 PR 12-MAR-1999; 99US-0123957.  
 PR 29-MAR-1999; 99US-0126773.  
 PR 21-APR-1999; 99US-0130232.  
 PR 28-APR-1999; 99US-0131445.  
 PR 14-MAY-1999; 99US-0134287.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 29-OCT-1999; 99US-0162506.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 02-DEC-1999; 99WO-US28551.  
 PR 02-DEC-1999; 99WO-US28565.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 30-DEC-1999; 99WO-US31243.  
 PR 30-DEC-1999; 99WO-US31274.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00277.  
 PR 06-JAN-2000; 2000WO-US00376.

XX (GETH ) GENENTECH INC.  
 XX  
 XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;  
 PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;  
 PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;  
 PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;  
 XX WPI; 2000-611443/58.  
 DR

DR N-PSDB; AAC78582.  
 XX Novel PRO polypeptides and polynucleotides used in detection methods;  
 PT to target bioactive molecules to specific cells, and to modulate  
 XX cellular activities  
 XX  
 PS Claim 12: Fig 207: 636pp; English.  
 XX  
 CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed  
 CC sequence tag) sequences which encode secreted or transmembrane PRO  
 CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic  
 CC activity. The polynucleotides and polypeptides can be used for detecting  
 CC the presence of PRO polypeptides in samples, for linking bioactive  
 CC molecules to cells and for modulating biological activities of cells,  
 CC using the polypeptides for specific targeting. The polypeptide targeting  
 CC can be used to kill the target cells, e.g. for the treatment of cancers.  
 CC the polypeptide pairs provide specific targeting of bioactive molecules  
 CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in  
 CC the isolation of the PRO polynucleotide sequences.  
 XX  
 SQ Sequence 345 AA;

Query Match 100.0%; Score 754; DB 21; Length 345;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-71;  
 Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDLEDLYRPTWQLGKAFVGRKSRVVDNLNLTTEVRLYSCTPRNFSVSIREELKRTDTI 60  
 Db 210 ldledlyrptwqlgkafvgrksrvvdnlnteervrlyscprnfsvsireelkrtdti 269  
 QY 61 FWPGGCLLVKRCGNCACCLHNCQCVPKSKYTKYHEVLQRLPKTGVRLHKLSTLTDVAL 120  
 Db 270 fwpgcllvkrcgncacclhncqcvpkskkyhevlqlrpkgtgvrghklsldval 329  
 QY 121 EHHEECDCVCRGSGTG 136  
 Db 330 ehheecdvcrgstgg 345

RESULT 9  
 AAB10633  
 ID AAB10633 standard; Protein; 345 AA.  
 XX  
 AC AAB10633;  
 XX  
 DT 19-JAN-2001 (first entry)  
 XX  
 DE Human RACE generated VEGF-X protein.  
 XX  
 KW VEGF-X; vascular endothelial growth factor; human; vulnery; cytostatic;  
 KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;  
 KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;  
 KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;  
 KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;  
 KW venous sore; diabetic ulcer; burns; skin graft growth.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200037641-A2.  
 XX  
 PD 29-JUN-2000.  
 XX  
 PF 21-DEC-1999; 99WO-US30503.  
 XX  
 PR 22-DEC-1998; 98GB-0028377.  
 PR 18-MAR-1999; 99US-0124967.  
 PR 08-NOV-1999; 99US-0164131.  
 XX  
 PA (JANC ) JANSEN PHARM NV.  
 XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JH, Gosiewska A;  
 PI Dhanaraj SN, Xu J;





```
XX 19-JAN-2001 (first entry)
XX Human VEGF-X protein #4.
DE VEGF-X; vascular endothelial growth factor; human; vulnery; cytostatic;
XX antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
KW venous sore; diabetic ulcer; burns; skin graft growth.
XX
XX Homo sapiens.
XX WO200037641-A2.
XX
XX 29-JUN-2000.
XX
XX 21-DEC-1999; 99WO-US30503.
XX
XX 22-DEC-1998; 98GB-0028377.
XX 18-MAR-1999; 99US-0124967.
XX 08-NOV-1999; 99US-0164131.
XX
XX (JANC ) JANSSEN PHARM NV.
XX
XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;
XX Dhanaraj SN, Xu J;
XX WPI: 2000-442669/38.
XX N-PSDB; AAA71990.
XX
XX New vascular endothelial growth factor protein, useful for treating or
XX preventing diseases associated with inappropriate angiogenesis activity
XX such as cancer, rheumatoid arthritis, psoriasis and wounds -
XX Disclosure; Fig 30B; 127pp; English.
XX
XX This invention describes a novel vascular endothelial growth factor-X
XX (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
XX vulnery, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
XX antidiabetic activity and acts as an angiogenesis and vascularization
XX regulator. An antisense molecule of the invention is useful for treating
XX or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
XX retinopathy by inhibiting angiogenic activity or inappropriate
XX vascularization including formation and proliferation of new blood
XX vessels, growth and development of tissues, tissue regeneration and organ
XX and tissue repair in a subject. The products of the invention are useful
XX for preparing medicaments for treating wounds such as dermal ulcers,
XX pressure sores, venous sores, diabetic ulcers and burns and to promote
XX skin graft growth, tissue repair, proliferation of new blood vessels,
XX tissue regeneration and organ repair by promoting angiogenic activity or
XX vascularization. This sequence represents a human VEGF-X protein
XX described in the method of the invention.
XX
XX Sequence 345 AA;
XX
XX Query Match 100.0%; Score 754; DB 21; Length 345;
XX Best Local Similarity 100.0%; Pred. No. 4.7e-71;
XX Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 LDLEDLYRPTWOLLGKAFVGRKSRVVDNLLTEEVRLYSCTPRNFVSIREELKRTDTI 60
DB 210 ldledlyrptwllgkafvgrksrvvdlntlteevrlyscprnfsvsireelkrttdi 269
QY 61 FWPGLLVKRCGNCACCLHNCNCCQVPSKVTKKYHEVLQLRPKTVGRGLHSLTDVAL 120
DB 270 fwpqllvkrccgncacclhncnccqvpksvktkyhevlqlrpkgtvrglhsltdval 329
QY 121 EHHECDVCVRGTGG 136
DB 330 ehhecdvcvrgstgg 345
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RESULT 14  
AAB10650  
ID AAB10650 standard; Protein; 345 AA.  
XX  
AC AAB10650;  
XX  
DT 19-JAN-2001 (first entry)  
XX  
DE Human 990126vegX protein.  
XX  
KW VEGF-X; vascular endothelial growth factor; human; vulnery; cytostatic;  
KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;  
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;  
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;  
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;  
KW venous sore; diabetic ulcer; burns; skin graft growth.  
XX  
OS Homo sapiens.  
XX  
PN WO200037641-A2.  
XX  
PD 29-JUN-2000.  
XX  
PF 21-DEC-1999; 99WO-US30503.  
XX  
PR 22-DEC-1998; 98GB-0028377.  
XX 18-MAR-1999; 99US-0124967.  
XX 08-NOV-1999; 99US-0164131.  
XX  
XX (JANC ) JANSSEN PHARM NV.  
XX  
XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;  
XX Dhanaraj SN, Xu J;  
XX WPI: 2000-442669/38.  
XX  
XX New vascular endothelial growth factor protein, useful for treating or  
XX preventing diseases associated with inappropriate angiogenesis activity  
XX such as cancer, rheumatoid arthritis, psoriasis and wounds -  
XX Disclosure; Fig 11; 127pp; English.  
XX  
XX This invention describes a novel vascular endothelial growth factor-X  
XX (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has  
XX vulnery, cytostatic, antirheumatic, antiarthritic, antipsoriatic and  
XX antidiabetic activity and acts as an angiogenesis and vascularization  
XX regulator. An antisense molecule of the invention is useful for treating  
XX or preventing cancer, rheumatoid arthritis, psoriasis and diabetic  
XX retinopathy by inhibiting angiogenic activity or inappropriate  
XX vascularization including formation and proliferation of new blood  
XX vessels, growth and development of tissues, tissue regeneration and organ  
XX and tissue repair in a subject. The products of the invention are useful  
XX for preparing medicaments for treating wounds such as dermal ulcers,  
XX pressure sores, venous sores, diabetic ulcers and burns and to promote  
XX skin graft growth, tissue repair, proliferation of new blood vessels,  
XX tissue regeneration and organ repair by promoting angiogenic activity or  
XX vascularization. This sequence represents the human 990126vegX protein  
XX used to illustrate the method of the invention.  
XX  
XX Sequence 345 AA;  
XX  
XX Query Match 100.0%; Score 754; DB 21; Length 345;  
XX Best Local Similarity 100.0%; Pred. No. 4.7e-71;  
XX Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 LDLEDLYRPTWOLLGKAFVGRKSRVVDNLLTEEVRLYSCTPRNFVSIREELKRTDTI 60  
DB 210 ldledlyrptwllgkafvgrksrvvdlntlteevrlyscprnfsvsireelkrttdi 269  
QY 61 FWPGLLVKRCGNCACCLHNCNCCQVPSKVTKKYHEVLQLRPKTVGRGLHSLTDVAL 120  
DB 270 fwpqllvkrccgncacclhncnccqvpksvktkyhevlqlrpkgtvrglhsltdval 329  
QY 121 EHHECDVCVRGTGG 136  
DB 330 ehhecdvcvrgstgg 345

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Db 270 fwpgccllvkrccgnacacclhncnecqcvpskvtkkyhevlqlrpkgtgvrghksltdval 329
Qy 121 EHHEECDCVCRGSTGG 136
Db 330 ehheecdcvcrgstgg 345

RESULT 15
AAB10651
ID AAB10651 standard; Protein; 345 AA.
AC AAB10651;
XX
DT 19-JAN-2001 (first entry)
DE Human VEGF-X protein #3.
XX
KW VEGF-X; vascular endothelial growth factor; human; vulnery; cytostatic;
KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
KW venous sore; diabetic ulcer; burns; skin graft growth.
XX
OS Homo sapiens.
XX
XX WO200037641-A2.
XX
XX 29-JUN-2000.
XX
XX 21-DEC-1999; 99WO-US30503.
XX
XX 22-DEC-1998; 98GB-0028377.
XX 18-MAR-1999; 99US-0124967.
XX 08-NOV-1999; 99US-0164131.
XX
XX (JANC ) JANSSEN PHARM NV.
XX
XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiowska A;
XX Dhanaraj SN, Xu J;
XX
XX WPI; 2000-442669/38.
XX
XX New vascular endothelial growth factor protein, useful for treating or
XX preventing diseases associated with inappropriate angiogenesis activity
XX such as cancer, rheumatoid arthritis, psoriasis and wounds -
XX
XX Claim 72; Fig 12; 127pp; English.
XX
XX This invention describes a novel vascular endothelial growth factor-X
XX (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
XX vulnery, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
XX antidiabetic activity and acts as an angiogenesis and vascularization
XX regulator. An antisense molecule of the invention is useful for treating
XX or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
XX retinopathy by inhibiting angiogenic activity or inappropriate
XX vascularization including formation and proliferation of new blood
XX vessels, growth and development of tissues, tissue regeneration and organ
XX and tissue repair in a subject. The products of the invention are useful
XX for preparing medicaments for treating wounds such as dermal ulcers,
XX pressure sores, venous sores, diabetic ulcers and burns and to promote
XX skin graft growth, tissue repair, proliferation of new blood vessels,
XX tissue regeneration and organ repair by promoting angiogenic activity or
XX vascularization. This sequence represents the human VEGF-X protein
XX described in the method of the invention.
XX
XX Sequence 345 AA;

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Query Match 100.0%; Score 754; DB 21; Length 345;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-71;  
 Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 LDLEDLYRPTWQLLGKAFVFGKSRVVDLNLITTEVRLYSCTPRNFSVSIREELKRTDTI 60
Db 210 ldledlyrptwqllgkafvfgkrsvvdnlitteevrlyscprnfsvsireelkrtdti 269
Qy 61 FWPGCCLLVKRCCGNACACCLHNCNCCQCVPSKVTKKYHEVLQLRPKGTGVRGLHKSITDVAL 120
Db 270 fwpgccllvkrccgnacacclhncnecqcvpskvtkkyhevlqlrpkgtgvrghksltdval 329
Qy 121 EHHEECDCVCRGSTGG 136
Db 330 ehheecdcvcrgstgg 345

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Search completed: August 18, 2001, 01:49:50  
 Job time: 2231 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 18, 2001, 01:15:44 ; Search time 54.67 Seconds  
(without alignments)  
51.222 Million cell updates/sec

Title: US-09-457-066-2\_COPY\_210\_345

Perfect score: 754

Sequence: 1 LDLEDLYRPTWQLGKAFV.....DVALEHHEBCDCVCRSTGG 136

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A.COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B.COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A.COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B.COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS.COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	119.5	15.8	321	4	US-08-915-795-9
2	119.5	15.8	358	4	US-08-915-795-8
3	116	15.4	325	4	US-08-915-795-3
4	116	15.4	354	4	US-08-915-795-5
5	114.5	15.2	256	6	5175255-9
6	110	14.6	190	3	US-08-867-352-25
7	110	14.6	220	6	5175255-4
8	110	14.6	241	1	US-08-387-845-4
9	110	14.6	241	2	US-08-999-811-6
10	110	14.6	241	2	US-08-778-275-4
11	110	14.6	241	2	US-08-824-996-8
12	110	14.6	241	3	US-08-989-251-29
13	110	14.6	241	3	US-09-042-105-6
14	110	14.6	241	3	US-08-867-352-4
15	110	14.6	241	3	US-09-340-250-29
16	110	14.6	241	4	US-08-795-430-54
17	110	14.6	241	5	PCT-US96-09001-9
18	110	14.6	241	6	5194596-15
19	110	14.6	241	6	5219739-15
20	107	14.2	205	3	US-08-989-251-27
21	107	14.2	205	3	US-08-989-251-37
22	107	14.2	205	3	US-09-340-250-27
23	107	14.2	205	3	US-09-340-250-37
24	105.5	14.0	188	1	US-08-469-427A-11
25	105.5	14.0	188	2	US-08-609-443B-11
26	105.5	14.0	188	2	US-08-569-063C-11
27	105.5	14.0	188	4	US-08-795-430-57

28 105.5 14.0 207 2 US-08-609-443B-15  
29 105.5 14.0 207 2 US-08-569-063C-15  
30 105 13.9 109 1 US-08-094-079-2  
31 105 13.9 109 1 US-08-094-079-3  
32 105 13.9 109 2 US-08-804-953-3  
33 105 13.9 109 3 US-08-691-794-4  
34 105 13.9 109 5 PCT-US91-02766-18  
35 105 13.9 109 5 PCT-US93-02612-1  
36 105 13.9 109 6 5498600-3  
37 105 13.9 119 2 US-08-257-494D-1  
38 105 13.9 120 6 5428135-2  
39 105 13.9 146 3 US-08-989-251-2  
40 105 13.9 146 3 US-08-989-251-25  
41 105 13.9 146 3 US-09-340-250-2  
42 105 13.9 146 3 US-09-340-250-25  
43 105 13.9 160 1 US-08-094-079-1  
44 105 13.9 282 1 US-08-445-847A-1  
45 104.5 13.9 109 3 US-08-691-794-3

#### ALIGNMENTS

RESULT 1  
US-08-915-795-9  
; Sequence 9, Application US/08915795  
; Patent No. 6235713  
; GENERAL INFORMATION:  
; APPLICANT: Marc G. ACHEN  
; APPLICANT: Andrew F. WILKS  
; APPLICANT: Steven A. STACKER  
; APPLICANT: Kari ALITALO  
; TITLE OF INVENTION: GROWTH FACTOR  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.  
; STREET: 1200 G Street, NW, Suite 700  
; CITY: Washington  
; STATE: DC  
; COUNTRY: United States of America  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/915,795  
; FILING DATE:  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: EVANS, Joseph D.  
; REGISTRATION NUMBER: 26,269  
; REFERENCE/DOCKET NUMBER: 1064/42983  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-8800  
; TELEFAX: (202) 628-8844  
; TELEX: N/A  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 321 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; TISSUE TYPE: Mouse Lung  
US-08-915-795-9

Query Match 15.8%; Score 119.5; DB 4; Length 321;  
Best Local Similarity 33.3%; Pred. No. 2e+05;  
Matches 36; Conservative 15; Mismatches 42; Indels 15; Gaps 6;



QY 29 LNLTEEVRLYSCTPRNFVSIREEL-KRTDTIFWPGCLLVKRCGNCACCLHNCNECQC 87  
Db 99 LKVIDEEMORTQCSPRETCVEASELGKTTNTFFKPPCVNVFRCGG---CC---NEEGVMC 153  
QY 88 V---PSKVTYKHYEVLQRLPKTGVRGLKSLTDVALEHHEECDCVCRG 132  
Db 154 MNTSTSYISKQLFEISV--PLTSV----PELVPKVIANHTGCKCLPTG 195

## RESULT 2

US-08-915-795-8  
; Sequence 8, Application US/08915795  
; Patent No. 6235713  
; GENERAL INFORMATION:  
; APPLICANT: Marc G. ACHEN  
; APPLICANT: Andrew F. WILKS  
; APPLICANT: Steven A. STACKER  
; APPLICANT: Kari ALITALO  
; TITLE OF INVENTION: GROWTH FACTOR  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.  
; STREET: 1200 G Street, NW, Suite 700  
; CITY: Washington  
; STATE: DC  
; COUNTRY: United States of America  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/915,795  
; FILING DATE:  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: EVANS, Joseph D.  
; REGISTRATION NUMBER: 26,269  
; REFERENCE/DOCKET NUMBER: 1064/42983  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-8800  
; TELEFAX: (202) 628-8844  
; TELEX: N/A  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 358 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; TISSUE TYPE: Mouse Lung  
; US-08-915-795-8

Query Match 15.8%; Score 119.5; DB 4; Length 358;  
Best Local Similarity 33.3%; Pred. No. 2.3e-05;  
Matches 36; Conservative 15; Mismatches 42; Indels 15; Gaps 6;

QY 29 LNLTEEVRLYSCTPRNFVSIREEL-KRTDTIFWPGCLLVKRCGNCACCLHNCNECQC 87  
Db 104 LKVIDEEMORTQCSPRETCVEASELGKTTNTFFKPPCVNVFRCGG---CC---NEEGVMC 158  
QY 88 V---PSKVTYKHYEVLQRLPKTGVRGLKSLTDVALEHHEECDCVCRG 132  
Db 159 MNTSTSYISKQLFEISV--PLTSV----PELVPKVIANHTGCKCLPTG 200

## RESULT 3

US-08-915-795-3  
; Sequence 3, Application US/08915795

; Patent No. 6235713  
; GENERAL INFORMATION:  
; APPLICANT: Marc G. ACHEN  
; APPLICANT: Andrew F. WILKS  
; APPLICANT: Steven A. STACKER  
; APPLICANT: Kari ALITALO  
; TITLE OF INVENTION: GROWTH FACTOR  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.  
; STREET: 1200 G Street, NW, Suite 700  
; CITY: Washington  
; STATE: DC  
; COUNTRY: United States of America  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/915,795  
; FILING DATE:  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: EVANS, Joseph D.  
; REGISTRATION NUMBER: 26,269  
; REFERENCE/DOCKET NUMBER: 1064/42983  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-8800  
; TELEFAX: (202) 628-8844  
; TELEX: N/A  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 325 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ORIGINAL SOURCE:  
; TISSUE TYPE: Human Breast  
; US-08-915-795-3

Query Match 15.4%; Score 116; DB 4; Length 325;  
Best Local Similarity 28.3%; Pred. No. 4.9e-05;  
Matches 43; Conservative 19; Mismatches 56; Indels 34; Gaps 8;

QY 3 LEDLYRPT---WQL-----LGRAVFGRKSR-----VVDLNLITFEVRLY 39  
Db 21 LEEELRITHSEDKWLKRLKLSFTSMDSRSASHSTRFAATFYDIETLKVIDEEMQRT 80  
QY 40 SCTPRNFVSIREEL-KRTDTIFWPGCLLVKRCGNCACCLHNCNEC-QCVPSKVTYKHY 97  
Db 81 QCSPRETCVEASELGKSTNTFFKPPCVNVFRCGG---CCNEESLICMNTSTSYISKQLF 137  
QY 98 EVLQRLPKTGVRGLKSLTDVALEHHEECDCV 129  
Db 138 EISV--PLTSV----PELVPKVIANHTGCKCL 163

## RESULT 4

US-08-915-795-5  
; Sequence 5, Application US/08915795  
; Patent No. 6235713  
; GENERAL INFORMATION:  
; APPLICANT: Marc G. ACHEN  
; APPLICANT: Andrew F. WILKS  
; APPLICANT: Steven A. STACKER  
; APPLICANT: Kari ALITALO  
; TITLE OF INVENTION: GROWTH FACTOR  
; NUMBER OF SEQUENCES: 11

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.  
;; STREET: 1200 G Street, NW, Suite 700  
;; CITY: Washington  
;; STATE: DC  
;; COUNTRY: United States of America  
;; ZIP: 20005  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/915,795  
;; FILING DATE:  
;; CLASSIFICATION: 536  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: EVANS, Joseph D.  
;; REGISTRATION NUMBER: 26,269  
;; REFERENCE/DOCKET NUMBER: 1064/42983  
;; TELEPHONE: (202) 628-8800  
;; TELEFAX: (202) 628-8844  
;; TELEX: N/A  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 354 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; HYPOTHETICAL: NO  
;; ORIGINAL SOURCE:  
;; TISSUE TYPE: Human Lung  
;;  
US-08-915-795-5

Query Match 15.4%; Score 116; DB 4; Length 354;  
Best Local Similarity 28.3%; Pred. No. 5.4e-05;  
Matches 43; Conservative 19; Mismatches 56; Indels 34; Gaps 8;

QY 3 LEDLYRPT-----WQL-----LGKAFVGRKSR-----VVDLNLLEEVRLY 39  
DB 50 LLELLRITHSDKMLRCLRLKLSFTSMDRSASHRSTRFAATFYDIETLKVIDEEMQRT 109  
QY 40 SCTPRNFVSIREL-KRTDTIFWPGCLLVKRCGNCACCLHNCNEC-QCVPKSVTKKYH 97  
DB 110 QCSPTCTVEVASELKGKSTNFFKPCVNVFRCGG-----CCNEESLICMTSTYSISKOLF 166  
QY 98 EVLQRPKTVGRGLHKSLLTDVALEHHEECDCV 129  
DB 167 EISV--PLTSV-----PELVPKVANHTGCKCL 192

RESULT 5  
5175255-9  
; Patent No. 5175255  
; APPLICANT: Thomason, Arlen R.; Nicholson, Margery  
; TITLE OF INVENTION: METHODS FOR PURIFICATION OF PLATELET-  
; DERIVED FACTOR  
; NUMBER OF SEQUENCES: 9  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/06/25,344  
; FILING DATE: 23-MAR-1987  
; SEQ ID NO: 9:  
; LENGTH: 256  
5175255-9

Query Match 15.2%; Score 114.5; DB 6; Length 256;  
Best Local Similarity 34.4%; Pred. No. 5.3e-05;  
Matches 45; Conservative 9; Mismatches 36; Indels 41; Gaps 10;

QY 12 QLLGKAF-----VFGKSRVVD-LNLLTEEV--RLYCTPRNFVSIREELKRTDTIFWPG 64  
DB 92 QYLSKVFTNNLVFGTSDRVFEKRLKLEEGISRLIDRTNANFLV-----WPP 138  
QY 65 CLLVKRCGNCACCLHNCNECQCPKSVTKKYHEVLQLRP-----KTGV---RGLHKSLLTD 117  
DB 139 CVEVORCSG---CC--NNRNVCQRPTQV-----QLRPVQVRKIEIVRKPFIRKAT- 184  
QY 118 VALEHHEECDC 128  
DB 185 VTLEDHLACKC 195  
RESULT 6  
US-08-867-352-25  
; Sequence 25, Application US/08867352  
; Patent No. 6060273  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Multicistronic expression units and their use  
; NUMBER OF SEQUENCES: 25  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPA)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/867,352  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/387,847  
; FILING DATE:  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 190 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-867-352-25

Query Match 14.6%; Score 110; DB 3; Length 190;  
Best Local Similarity 32.9%; Pred. No. 0.00012;  
Matches 46; Conservative 13; Mismatches 37; Indels 44; Gaps 12;

QY 2 DLEDLYRPTWQLLGKAFVFGKSRVVDLNLTT--EVRLYSCTPRN--FSVSIREELKRT 57  
DB 72 ELESRLAR-----GRRS---LGLATAEPAMIAECKTRTEVEFEIS--RRLIDRT 114  
QY 58 DTIF--WPGCLLVKRCGNCACCLHNCNECQCPKSVTKKYHEVLQLRP-----KTGV--- 108  
DB 115 NANFLVWPPCQVEVQRCSG---CC--NNRNVCQRPTQV-----QLRPVQVRKIEIVRK 161  
QY 109 RGLHKSLLTDVALEHHEECDC 128  
DB 162 KPDKKAT-VTLEDHLACKC 180

RESULT 7  
5175255-4  
; Patent No. 5175255  
; APPLICANT: Thomason, Arlen R.; Nicholson, Margery  
; TITLE OF INVENTION: METHODS FOR PURIFICATION OF PLATELET-  
; DERIVED GROWTH FACTOR  
; NUMBER OF SEQUENCES: 9  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/06/25,344  
; FILING DATE: 23-MAR-1987  
; SEQ ID NO: 4:  
; LENGTH: 220  
5175255-4

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Query Match      14.6%; Score 110; DB 6; Length 220;
Best Local Similarity 32.9%; Pred. No. 0.00014;
Matches 46; Conservative 13; Mismatches 37; Indels 44; Gaps 12;

QY 2 DLEDLYRPTWLLGKAFVGRKSRVVDNLNLT--EEVRLYSCTPRN--FVSISIREELKRT 57
   :||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 51 ELESAR-----GRRS-----LGSITIAEPAMIAECKTRTEVFEIS--RRLDRT 93

QY 58 DTIF--WPGCLLVKRCGGNACCLHNCQCVPKVKYKHYEVQLRP-----KTGV--- 108
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 94 NANFLVMPPCVEVQRCSG---CC--NNRNVCQRPQV-----QLRPVQVRKIEIVRK 140

QY 109 RGLHKSITDVALEHHECDC 128
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 141 KPFFKAT-VTLEDHLACKC 159

RESULT 8
US-08-387-845-4
; Sequence 4, Application US/08387845
; Patent No. 5665567
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Preparation of heterodimeric PDGF-AB using a
; bicistronic vector system in mammalian cells
; NUMBER OF SEQUENCES: 16
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPA)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,845
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-387-845-4

Query Match      14.6%; Score 110; DB 1; Length 241;
Best Local Similarity 32.9%; Pred. No. 0.00015;
Matches 46; Conservative 13; Mismatches 37; Indels 44; Gaps 12;

QY 2 DLEDLYRPTWLLGKAFVGRKSRVVDNLNLT--EEVRLYSCTPRN--FVSISIREELKRT 57
   :||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 72 ELESAR-----GRRS-----LGSITIAEPAMIAECKTRTEVFEIS--RRLDRT 114

QY 58 DTIF--WPGCLLVKRCGGNACCLHNCQCVPKVKYKHYEVQLRP-----KTGV--- 108
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 115 NANFLVMPPCVEVQRCSG---CC--NNRNVCQRPQV-----QLRPVQVRKIEIVRK 161

QY 109 RGLHKSITDVALEHHECDC 128
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 162 KPFFKAT-VTLEDHLACKC 180

RESULT 9
US-08-999-811-6
; Sequence 6, Application US/08999811
; Patent No. 5932540
; GENERAL INFORMATION:
; APPLICANT: HU, JING-SHAN
; APPLICANT: ROSEN, CRAIG A.
; APPLICANT: CAO, LIANG
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 NEW YORK AVENUE
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/999,811
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/207,550
; FILING DATE: 8-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,968
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MARKOWICZ, KAREN R.
; REGISTRATION NUMBER: 36,351
; REFERENCE/DOCKET NUMBER: 1488.1000004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; US-08-999-811-6

Query Match      14.6%; Score 110; DB 2; Length 241;
Best Local Similarity 32.9%; Pred. No. 0.00015;
Matches 46; Conservative 13; Mismatches 37; Indels 44; Gaps 12;

QY 2 DLEDLYRPTWLLGKAFVGRKSRVVDNLNLT--EEVRLYSCTPRN--FVSISIREELKRT 57
   :||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 72 ELESAR-----GRRS-----LGSITIAEPAMIAECKTRTEVFEIS--RRLDRT 114

QY 58 DTIF--WPGCLLVKRCGGNACCLHNCQCVPKVKYKHYEVQLRP-----KTGV--- 108
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 115 NANFLVMPPCVEVQRCSG---CC--NNRNVCQRPQV-----QLRPVQVRKIEIVRK 161

QY 109 RGLHKSITDVALEHHECDC 128
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 162 KPFFKAT-VTLEDHLACKC 180

RESULT 10
US-08-778-275-4
; Sequence 4, Application US/08778275
; Patent No. 5935819
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Preparation of heterodimeric PDGF-AB using a
; bicistronic vector system in mammalian cells
; NUMBER OF SEQUENCES: 16
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPA)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/778,275
; FILING DATE:
; CLASSIFICATION:
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US-08-389-231-29  
: Sequence 29, Application US/08989251

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/042,105  
FILING DATE: HEREMITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/207,550  
FILING DATE: 8-MAR-1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/465,968  
FILING DATE: 06-JUN-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: TO BE ASSIGNED  
FILING DATE: 24-DEC-1997  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: ERIC K. STEFFE  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488.1000003/EKS  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)371-2600  
TELEFAX: (202)371-2540  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: not relevant  
MOLECULE TYPE: protein  
US-09-042-105-6

Query Match 14.6%; Score 110; DB 3; Length 241;  
Best Local Similarity 32.9%; Pred. No. 0.00015;  
Matches 46; Conservative 13; Mismatches 37; Indels 44; Gaps 12;  
QY 2 DLEDLYRPTWQLLGKAFVGRKSRVVDNLIT--EEVRLYSCTPRN--FVSISREELKRT 57  
Db 72 ELESAR-----GRRS-----LGSLTAEAPAMIAECKTRTEVFEIS--RRLIDRT 114  
QY 58 DTIF--WPGCLLVKRGNCACCLHNCNECQVPSKVKYHEVLQLRP---KTGV--- 108  
Db 115 NANFLVMPPCVEVORCSG---CC--NNRNVQCRPTQV-----QLRPVQVRKIEIVRK 161  
QY 109 RGLHKSITDVALEHHECDC 128  
Db 162 KPIFKKAT-VTLEDHLACKC 180

RESULT 14  
US-08-867-352-4  
Sequence 4, Application US/08867352  
Patent No. 6060273  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Multicistronic expression units and their use  
NUMBER OF SEQUENCES: 25  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPA)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/867,352  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/387,847

FILING DATE:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-867-352-4  
Query Match 14.6%; Score 110; DB 3; Length 241;  
Best Local Similarity 32.9%; Pred. No. 0.00015;  
Matches 46; Conservative 13; Mismatches 37; Indels 44; Gaps 12;  
QY 2 DLEDLYRPTWQLLGKAFVGRKSRVVDNLIT--EEVRLYSCTPRN--FVSISREELKRT 57  
Db 72 ELESAR-----GRRS-----LGSLTAEAPAMIAECKTRTEVFEIS--RRLIDRT 114  
QY 58 DTIF--WPGCLLVKRGNCACCLHNCNECQVPSKVKYHEVLQLRP---KTGV--- 108  
Db 115 NANFLVMPPCVEVORCSG---CC--NNRNVQCRPTQV-----QLRPVQVRKIEIVRK 161  
QY 109 RGLHKSITDVALEHHECDC 128  
Db 162 KPIFKKAT-VTLEDHLACKC 180

RESULT 15  
US-09-340-250-29  
Sequence 29, Application US/09340250  
Patent No. 6083723  
GENERAL INFORMATION:  
APPLICANT: Tekamp-Olson, Patricia  
TITLE OF INVENTION: METHOD FOR EXPRESSION OF HETEROLOGOUS  
TITLE OF INVENTION: PROTEINS IN YEAST  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bell Seltzer IP Group of Alston & Bird, LLP  
STREET: 3605 Glenwood Ave. Suite 310  
CITY: Raleigh  
STATE: NC  
COUNTRY: US  
ZIP: 27622  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/340,250  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/989,251  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Spruill, W. Murray  
REGISTRATION NUMBER: 32,943  
REFERENCE/DOCKET NUMBER: 5784-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919 420 2202  
TELEFAX: 919 881 3175  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-340-250-29

Query Match 14.6%; Score 110; DB 3; Length 241;  
Best Local Similarity 32.9%; Pred. No. 0.00015;



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 18, 2001, 01:36:44 ; Search time 58.9 Seconds  
(without alignments)  
175.887 Million cell updates/sec

Title: US-09-457-066-2\_COPY\_210\_345  
Perfect score: 754  
Sequence: 1 LDLEDLYRPTWQLLGKARVF.....DVALEHHECDVCVCRGSGG 136  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

PIR\_68:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	114.5	15.2	148	D49530	16K vascular endothelial growth factor homolog A2R - Orf virus
2	110	14.6	166	JN0248	platelet-derived growth factor chain A3 precursor - rabbit (fragment)
3	110	14.6	198	JS0735	platelet-derived growth factor chain A3 precursor - rabbit (fragment)
4	110	14.6	241	PFHUG2	platelet-derived growth factor chain A3 precursor - rabbit (fragment)
5	108	14.3	200	I51551	platelet-derived growth factor chain A3 precursor - rabbit (fragment)
6	108	14.3	215	S08220	platelet-derived growth factor chain A3 precursor - rabbit (fragment)
7	108	14.3	226	I51550	platelet-derived growth factor chain A3 precursor - rabbit (fragment)
8	107	14.2	245	TVCYSS	platelet-derived growth factor chain A3 precursor - rabbit (fragment)
9	104.5	13.9	232	A41551	vascular endothelial growth factor chain A3 precursor - rabbit (fragment)
10	104	13.8	196	B28964	platelet-derived growth factor chain A3 precursor - rabbit (fragment)
11	104	13.8	197	S25096	platelet-derived growth factor chain A3 precursor - rabbit (fragment)
12	104	13.8	211	PFHUG1	platelet-derived growth factor chain A3 precursor - rabbit (fragment)
13	104	13.8	226	TVMYSS	platelet-derived growth factor chain A3 precursor - rabbit (fragment)
14	102.5	13.6	133	B49530	platelet-derived growth factor chain A3 precursor - rabbit (fragment)
15	102.5	13.6	190	S52130	platelet-derived growth factor chain A3 precursor - rabbit (fragment)
16	102.5	13.6	196	A37359	platelet-derived growth factor chain A3 precursor - rabbit (fragment)
17	102.5	13.6	196	A48951	platelet-derived growth factor chain A3 precursor - rabbit (fragment)
18	102.5	13.6	419	S69207	platelet-derived growth factor chain A3 precursor - rabbit (fragment)
19	101.5	13.5	120	A33787	platelet-derived growth factor chain A3 precursor - rabbit (fragment)
20	101.5	13.5	146	S57956	platelet-derived growth factor chain A3 precursor - rabbit (fragment)
21	101.5	13.5	190	B40080	platelet-derived growth factor chain A3 precursor - rabbit (fragment)
22	97	12.9	188	JC4680	platelet-derived growth factor chain A3 precursor - rabbit (fragment)
23	97	12.9	207	JC4679	platelet-derived growth factor chain A3 precursor - rabbit (fragment)
24	96.5	12.8	190	A35987	platelet-derived growth factor chain A3 precursor - rabbit (fragment)
25	95.5	12.7	190	B44881	platelet-derived growth factor chain A3 precursor - rabbit (fragment)
26	95.5	12.7	214	A44881	platelet-derived growth factor chain A3 precursor - rabbit (fragment)
27	94	12.5	225	S25097	platelet-derived growth factor chain A3 precursor - rabbit (fragment)
28	94	12.5	241	PFMSGB	platelet-derived growth factor chain A3 precursor - rabbit (fragment)
29	88	11.7	271	A25669	platelet-derived growth factor chain A3 precursor - rabbit (fragment)

RESULT 1  
D49530  
16K vascular endothelial growth factor homolog A2R - Orf virus  
C:Species: Orf virus  
C:Date: 07-Apr-1994 #sequence\_revision 18-Nov-1994 #text\_change 08-Oct-1999  
C:Accession: D49530  
R:Lytle, D.J.; Fraser, K.M.; Fleming, S.B.; Mercer, A.A.; Robinson, A.J.  
J. Virol. 68, 84-92, 1994  
A:Title: Homologs of vascular endothelial growth factor are encoded by the poxvirus o  
A:Reference number: A49530; MUID:94076465  
A:Contents: NZ  
A:Status: preliminary  
A:Accession: D49530  
A:Molecule type: DNA  
A:Residues: 1-148 <LYT>  
A:Cross-references: GB:S67522; NID:9456900; PIDN:AAH29223.1; PID:9456902  
A:Note: sequence extracted from NCBI backbone (NCBIN:141422, NCBI:141426)

#### ALIGNMENTS

Query Match 15.2%; Score 114.5; DB 2; Length 148;  
Best Local Similarity 30.2%; Pred. No. 0.00047;  
Matches 29; Conservative 19; Mismatches 43; Indels 5; Gaps 3;  
Qy 41 CTPNFSVSIREL-KRTDTIEWPGCLLVKRGCCACCLHNCNEQCQVPSVKYKHYEV 99  
Db 46 CAPRDTVVTLGEYPESTNLQNPRTVTKRSG---CCNGDQICTAVETRTVTVS 102  
Qy 100 LQLRPTGYR-GLHKSLTDVALEHHECDVCVCRGST 134  
Db 103 TGVSSSGTNGSVSTNLQRISVTEHTKDCIGRTTT 138

#### RESULT 2

JN0248  
platelet-derived growth factor chain A3 precursor - rabbit (fragment)  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 27-Jun-1994  
C:Accession: JN0248  
R:Nakamura, H.; Kuro-O, M.; Takewaki, S.; Iwase, M.; Ohkubo, A.; Yazak  
Biochem. Biophys. Res. Commun. 184, 811-818, 1992  
A:Title: Identification of three types of PDGF-A chain gene transcripts in rabbit vas  
A:Reference number: JN0248; MUID:92246970  
A:Accession: JN0248  
A:Molecule type: mRNA  
A:Residues: 1-166 <NAK>  
C:Superfamily: platelet-derived growth factor  
F:1-22/Domain: propeptide (fragment) #status predicted <PRO>  
F:23-166/Product: platelet-derived growth factor A3 chain #status predicted <MAT>

Query Match 14.6%; Score 110; DB 2; Length 166;  
Best Local Similarity 30.5%; Pred. No. 0.0014;





A:Residues: 'SLSL', 17-20, 'RQ', 22-241 <JOH>  
A:Cross-references: GB:X00556; GB:X00559; GB:X00560; GB:X00561; GB:X00562  
R:Dirks, R.P.H.; Onnekink, C.; Jansen, H.J.; de Jong, A.; Bloemers, H.P.J.  
Nucleic Acids Res. 23, 2815-2822, 1995  
A:Title: A novel human c-sis mRNA species is transcribed from a promoter in c-sis intron  
A:Reference number: S58382; MUID:95388493  
A:Accession: S58383  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 'MFINGL', 22-200 <DIR>  
A:Cross-references: EMBL:X83705; NID:9951023; PIDN:CAA58679.1; PID:9951025  
R:Cook, A.L.; Kirwin, P.M.; Craig, S.; Bawden, L.J.; Green, D.R.; Price, M.J.; Richards  
Biochem. J. 281, 57-65, 1992  
A:Title: Purification and analysis of proteinase-resistant mutants of recombinant platelet  
A:Reference number: I38108; MUID:92117992  
A:Accession: I38108  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 'M', 82-241 <COO>  
A:Cross-references: EMBL:X83966; NID:9311378; PIDN:CAA45383.1; PID:935377  
A:Note: mutagenized recombinant sequence  
C:Comment: Platelet-derived growth factor, a potent mitogen for cells of mesenchymal origin  
C:Genetics:  
A:Gene: GDB:PDGFB  
A:Cross-references: GDB:120709; OMIM:190040  
A:Map position: 22q12.3-22q13.1  
A:Introns: 57/3; 94/1; 192/3; 241/1  
C:Complex: homodimer; heterodimer (see PIR:PFHUG1)  
C:Superfamily: platelet-derived growth factor  
C:Keywords: growth factor; mitogen  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-81/Domain: amino-terminal propeptide #status predicted <PRO>  
F:82-190/Product: platelet-derived growth factor chain B #status experimental <MAT>  
F:159-163/Region: receptor binding #status predicted  
F:191-241/Domain: carboxyl-terminal propeptide #status predicted <CTP>  
F:97-141,130-178,134-180/Disulfide bonds: #status experimental  
F:124/Disulfide bonds: interchain (to 133 in homodimeric form) #status experimental  
F:124/Disulfide bonds: interchain (to chain A-132 in heterodimeric form) #status predicted  
F:133/Disulfide bonds: interchain (to 124 in homodimeric form) #status experimental  
F:133/Disulfide bonds: interchain (to chain A-124 in heterodimeric form) #status predicted

Query Match 14.6%; Score 110; DB 1; Length 241;  
Best Local Similarity 32.9%; Pred. No. 0.002;  
Matches 46; Conservative 13; Mismatches 37; Indels 44; Gaps 12;  
QY 2 DLEDLYRPTWQLGKAFVGRKSRVVDNLIT--EEVRLYSCTPRN--FSVSIREELKRT 57  
Db 72 ELESAR-----GRRS-----LGSLTIAEPAMIAECKTTFEFTS--RRLDRT 114  
QY 58 DTIF--WPGCLLVKRCGNCACCLHNCNCCQVPSKVTKYHVLQRP---KTGV--- 108  
Db 115 NANFLWPPCVCVEQRCSG---CC--NNRNVCQRTQV-----QLRPQVRKIEIVRK 161  
QY 109 RGLHKSITDVALEHHECDC 128  
Db 162 KPIFKKAT-VTLEDHLACKC 180

RESULT 5  
I51551  
platelet-derived growth factor A chain short form precursor - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 16-Jul-1999  
C:Accession: I51551  
R:Mercola, M.; Melton, D.A.; Stiles, C.D.  
Science 241, 1223-1225, 1988  
A:Title: Platelet-derived growth factor A chain is maternally encoded in xenopus embryos  
A:Reference number: I51551; MUID:88321676  
A:Accession: I51551  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-200 <MER>

A:Cross-references: GB:M23238; NID:9214650; PIDN:AAA49928.1; PID:9214651  
C:Superfamily: platelet-derived growth factor

Query Match 14.3%; Score 108; DB 2; Length 200;  
Best Local Similarity 30.8%; Pred. No. 0.0027;  
Matches 40; Conservative 15; Mismatches 43; Indels 32; Gaps 9;  
QY 16 KAFVFGKRSRVVDNLNLTTEVRLYSCTPRNFSVSI--REELKRTDTIF--WPGCLLVKRCG 72  
Db 82 KRSVPSPRRKRSV-----EEAVPAICKTRTVIVEIPRSQIDPTSANFLIWPCCVEVKRCT 135  
QY 73 GNCACCLHNCNCCQVPSKVTKYH-----EVLQRPKTVGRGLHKSITDVALEHHE 124  
Db 136 G---CC--NTSSVKCQPSRI---HHRSVKAVKVEYVRKKPK-----LKEVL--VRLEHL 180  
QY 125 ECDVCVCGST 134  
Db 181 ECTCTANSNS 190

RESULT 6  
S08220  
platelet-derived growth factor chain A precursor - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 16-Jul-1999  
C:Accession: S08220  
R:Bejcek, B.E.; Li, D.Y.; Deuel, T.F.  
Nucleic Acids Res. 18, 680, 1990  
A:Title: Nucleotide sequence of a cDNA clone of Xenopus platelet-derived growth factor  
A:Reference number: S08220; MUID:90175018  
A:Accession: S08220  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-215 <BEJ>  
A:Cross-references: EMBL:X17545; NID:964973; PIDN:CAA35583.1; PID:964974  
C:Superfamily: platelet-derived growth factor  
C:Keywords: alternative splicing; growth factor  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-91/Domain: propeptide #status predicted <PRO>  
F:92-215/Product: platelet-derived growth factor chain A #status predicted <MAT>

Query Match 14.3%; Score 108; DB 2; Length 215;  
Best Local Similarity 30.8%; Pred. No. 0.0028;  
Matches 40; Conservative 15; Mismatches 43; Indels 32; Gaps 9;  
QY 16 KAFVFGKRSRVVDNLNLTTEVRLYSCTPRNFSVSI--REELKRTDTIF--WPGCLLVKRCG 72  
Db 82 KRSVPSPRRKRSV-----EEAVPAICKTRTVIVEIPRSQIDPTSANFLIWPCCVEVKRCT 135  
QY 73 GNCACCLHNCNCCQVPSKVTKYH-----EVLQRPKTVGRGLHKSITDVALEHHE 124  
Db 136 G---CC--NTSSVKCQPSRI---HHRSVKAVKVEYVRKKPK-----LKEVL--VRLEHL 180  
QY 125 ECDVCVCGST 134  
Db 181 ECTCTANSNS 190

RESULT 7  
I51550  
platelet-derived growth factor A chain long form precursor - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 16-Jul-1999  
C:Accession: I51550  
R:Mercola, M.; Melton, D.A.; Stiles, C.D.  
Science 241, 1223-1225, 1988  
A:Title: Platelet-derived growth factor A chain is maternally encoded in Xenopus embr  
A:Reference number: I51550; MUID:88321676  
A:Accession: I51550  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA

Mol. Endocrinol. 5, 1806-1814, 1991  
A:Title: The vascular endothelial growth factor family: identification of a fourth member  
A:Reference number: A41551; MUID:92168017  
A:Accession: A41551  
A:Molecule type: mRNA  
A:Residues: 1-232 <HOU1>  
A:Cross-references: GB:S85192; NID:g246155; PID:g246156  
A:Accession: C41551  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-140, 'N', 183-232 <HOU2>  
A:Accession: B41551  
A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-141, 227-232 <HOU>  
R:Tischer, E.; Mitchell, R.; Hartman, T.; Silva, M.; Gospodarowicz, D.; Fiddes, J.C.; J. Biol. Chem. 266, 11947-11954, 1991  
A:Title: The human gene for vascular endothelial growth factor. Multiple protein forms  
A:Reference number: A40454; MUID:91268072  
A:Accession: A40454  
A:Molecule type: DNA  
A:Residues: 1-165, 183-232 <TI1>  
A:Cross-references: GB:M63971; GB:M63972; GB:M63973; GB:M63974; GB:M63975; GB:M63976;  
A:Accession: B40454  
A:Molecule type: DNA  
A:Residues: 1-140, 'N', 183-232 <TI2>  
A:Cross-references: GB:M63971; GB:M63972; GB:M63973; GB:M63974; GB:M63975; GB:M63977;  
A:Accession: C40454  
A:Molecule type: DNA  
A:Residues: 1-141, 227-232 <TI3>  
A:Cross-references: GB:M63971; GB:M63972; GB:M63973; GB:M63974; GB:M63975; GB:M63978;  
R:Kock, P.J.; Hauser, S.D.; Krivi, G.; Sanzo, K.; Warren, T.; Feder, J.; Connolly, D. Science 246, 1309-1312, 1989  
A:Title: Vascular permeability factor, an endothelial cell mitogen related to PDGF.  
A:Reference number: A40079; MUID:90069609  
A:Accession: A40079  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-165, 183-232 <KEC>  
A:Cross-references: GB:M27281; NID:g340300; PIDN:AAA36807.1; PID:g340301  
R:Leung, D.W.; Cachianes, G.; Kiang, W.J.; Goeddel, D.V.; Ferrara, N. Science 246, 1306-1309, 1989  
A:Title: Vascular endothelial growth factor is a secreted angiogenic mitogen.  
A:Reference number: A40080; MUID:90069608  
A:Accession: A40080  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-140, 'N', 183-232 <LEU>  
A:Cross-references: GB:M32977; NID:g181970; PIDN:AAA35789.1; PID:g181971  
R:Weinzel, K.; Marme, D.; Welch, H.A. Biochem. Biophys. Res. Commun. 183, 1167-1174, 1992  
A:Title: AIDS-associated Kaposi's sarcoma cells in culture express vascular endothelial growth factor  
A:Reference number: JQ1463; MUID:92231879  
A:Accession: JQ1463  
A:Molecule type: mRNA  
A:Residues: 1-140, 'N', 183-232 <WE1>  
A:Cross-references: EMBL:X62568; NID:g37658; PIDN:CAA44447.1; PID:g37659  
A:Experimental source: AIDS-Kaposi's sarcoma cell  
A:Accession: JQ1464  
A:Molecule type: mRNA  
A:Residues: 1-140, 'N', 227-232 <WE2>  
A:Cross-references: AIDS-Kaposi's sarcoma cell  
R:Connolly, D.T.; Olander, J.V.; Heuvelman, D.; Nelson, R.; Monsell, R.; Siegel, N.; J. Biol. Chem. 264, 20017-20024, 1989  
A:Title: Human vascular permeability factor. Isolation from U937 cells.  
A:Reference number: A34492; MUID:90062112  
A:Accession: A34492  
A:Molecule type: protein  
A:Residues: 27-36, 43-49, 'R', 72-76, 'Q', 78-81, 59-71 <CON>  
C:Comment: The most common of several alternatively spliced forms is VEGF 165.  
C:Genetics:  
A:Gene: GDB:VEGF  
A:Cross-references: GDB:I32244; OMIM:192240

```

Db 151 KVAKVEYVRKKPKLKEV-----QVRLEHLEAC 179
      | : | : | : | : | : | : | : | : | : |
RESULT 11
S25096
platelet-derived growth factor chain A precursor - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
C:Accession: S25096; S3764
R:Herren, B.; Weyer, K.A.; Rouge, M.; Loetscher, P.; Pech, M.
submitted to the EMBL Data Library, July 1992
A:Description: Cross-species conservation in sequence and function of PDGF ligands and
A:Reference number: S25096
A:Accession: S25096
A:Molecule type: mRNA
A:Residues: 1-197 <HER1>
A:Cross-references: EMBL:Z14120; NID:g56865; PIDN:CAA78490.1; PID:g56866
R:Herren, B.; Weyer, K.A.; Rouge, M.; Loetscher, P.; Pech, M.
Biochim. Biophys. Acta 1173, 294-302, 1993
A:Title: Conservation in sequence and affinity of human and rodent PDGF ligands and
A:Reference number: S33764; MUID:93305723
A:Accession: S33764
A:Molecule type: mRNA
A:Residues: 89-172 <HER2>
A:Cross-references: EMBL:Z14120
C:Superfamily: platelet-derived growth factor
C:Keywords: growth factor; mitogen; platelet

Query Match 13.8%; Score 104; DB 2; Length 197;
Best Local Similarity 34.0%; Pred. No. 0.0064;
Matches 32; Conservative 12; Mismatches 34; Indels 16; Gaps 6;

QY 41 CTPRNFVSII-REELKRTDTIF--WPGCLLVKRCGGNCACCLHNCQCQVPSKV---TK 94
      | : | : | : | : | : | : | : | : | : |
Db 89 CKRTVIYEIPRSQVDPTSANFLIWPPCEVKRCTG---CC--NTSSVKQCPQSRVHRSV 143
      | : | : | : | : | : | : | : | : | : |
QY 95 KYHEVLQLRPRTGVRGLHKLSTDLVALEHHIECD 128
      | : | : | : | : | : | : | : | : | : |
Db 144 KVAKVEYVRKKPKLKEV-----QVRLEHLEAC 172
      | : | : | : | : | : | : | : | : | : |

RESULT 12
PFHUG1
Platelet-derived growth factor chain A precursor - human
N:Alternate names: PDGF A-chain; PDGF-1; PDGF-A; platelet-derived growth factor 1
C:Species: Homo sapiens (man)
C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 18-Feb-2000
C:Accession: A28964; S47564; A42002; A01379; S00173; A28122
R:Bonthron, D.T.; Morton, C.C.; Orkin, S.H.; Collins, T.
Proc. Natl. Acad. Sci. U.S.A. 85, 1492-1496, 1988
A:Title: Platelet-derived growth factor A chain: gene structure, chromosomal location
A:Reference number: A28964; MUID:88144463
A:Accession: A28964
A:Molecule type: DNA
A:Residues: 1-211 <BON>
A:Cross-references: GB:M21571; GB:J03638; GB:M19984; GB:M19985; GB:M19986; GB:M19987;
R:Takimoto, Y.; Kuramoto, A.
Biochim. Biophys. Acta 1222, 511-514, 1994
A:Title: Gene regulation by the 5'-untranslated region of the platelet-derived growth
A:Reference number: S47564; MUID:94312450
A:Accession: S47564
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-21 <TAK>
R:Bonthron, D.; Collins, T.; Grzeschik, K.H.; van Roy, N.; Speleman, F.
Genomics 13, 257-263, 1992
A:Title: Platelet-derived growth factor A chain: confirmation of localization of PDGF
A:Reference number: A42002; MUID:92307656
A:Accession: A42002
A>Status: preliminary
A:Molecule type: DNA
A:Molecule type: not compared with conceptual translation

```

A:Residues: 152-211 <B02>  
R:Betscholtz, C.; Johnson, A.; Heldin, C.H.; Westermark, B.; Lind, P.; Urdea, M.S.; Eddy  
Nature 320, 695-699, 1986  
A:Title: cDNA sequence and chromosomal localization of human platelet-derived growth fac  
A:Reference number: A01379; MUID:86203630  
A:Accession: A01379  
A:Molecule type: mRNA  
A:Residues: 1-211 <B01>  
A:CROSS-references: GB:X03795; NID:g35365; PIDN:CAA27421.1; PID:g35366  
A:Experimental source: clonal glioma cell line U-343 MGAC12.6, a tumor cell line  
R:Hoppe, J.; Schumacher, L.; Eichner, W.; Welch, H.A.  
FEBS Lett. 223, 243-246, 1987  
A:Title: The long 3'-untranslated regions of the PDGF-A and -B mRNAs are only distantly  
A:Reference number: S00173; MUID:88030061  
A:Accession: S00173  
A:Molecule type: mRNA  
A:Residues: 1-193, 'DVR' <HOP>  
A:CROSS-references: EMBL:X06374; NID:g35363; PIDN:CAA29677.1; PID:g35364  
R:Rorsman, F.; Bywater, M.; Knott, T.J.; Scott, J.; Betscholtz, C.  
Mol. Cell. Biol. 8, 571-577, 1988  
A:Title: Structural characterization of the human platelet-derived growth factor A-chain  
A:Reference number: A28122; MUID:88174698  
A:Accession: A28122  
A:Molecule type: mRNA  
A:Residues: 1-63, 'TRD', 67-211 <ROR>  
A:CROSS-references: GB:M20488  
A:Note: the authors translated the codon ACA for residue 64 as Arg, CGT for residue 65 a  
C:Comment: Platelet-derived growth factor, a potent mitogen for cells of mesenchymal ori  
C:Comment: A carboxyl-terminal propeptide may be removed from the precursor by proteolys  
C:Genetics:  
A:Gene: GDB:PDGFA  
A:CROSS-references: GDB:I20266; OMIM:173430  
A:Map position: 7p22-7p22  
A:Introns: 21/3; 54/1; 89/1; 151/3; 194/1  
C:Complex: homodimer; heterodimer (see PIR:PRHUG2)  
C:Superfamily: platelet-derived growth factor  
C:Keywords: alternative splicing; glycoprotein; growth factor; mitogen; platelet  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-86/Domain: propeptide #status predicted <PRO>  
F:87-211/Product: platelet-derived growth factor chain A #status predicted <MAT>  
F:158-162/Region: receptor binding #status predicted  
F:96-140, 129-177, 133-179/Disulfide bonds: #status predicted  
F:123/Disulfide bonds: interchain (to chain B-133 in heterodimeric form) #status predict  
F:123/Disulfide bonds: interchain (to 132 in homodimeric form) #status predicted  
F:132/Disulfide bonds: interchain (to chain B-124 in heterodimeric form) #status predict  
F:132/Disulfide bonds: interchain (to 123 in homodimeric form) #status predicted  
F:134/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 13.8%; Score 104; DB 1; Length 211;  
Best Local Similarity 34.0%; Pred. No. 0.0069;  
Matches 32; Conservative 12; Mismatches 34; Indels 16; Gaps 6;  
QY 41 CTPRNFVSII-REELKRYDTIF--WPGCLLVKRCGNCACCLHNCNECQVPSKV---TK 94  
DB 96 CKTRVVIETPRNSQVDPSTANFLIMPVPCVEVRCRG---CC---NTSSVRKQPSRVHRSV 150  
QY 95 KYHEVLQRLPKTGVRGLHKSILTDVALEHHEECDC 128  
DB 151 KVAKVEYVRKKPKLKEV-----QVRLEHLEAC 179  
RESULT 13  
TVMVSS  
PDGF-related transforming protein (sis) - simian sarcoma virus  
N:Alternate names: p28-sis  
C:Species: simian sarcoma virus  
C:Accession: A01381  
C:Date: 23-Jul-1983 #sequence\_revision 20-Sep-1984 #text\_change 31-Oct-1997  
R:Devare, S.G.; Reddy, E.P.; Law, J.D.; Robbins, K.C.; Aaronson, S.A.  
Proc. Natl. Acad. Sci. U.S.A. 80, 731-735, 1983  
A:Title: Nucleotide sequence of the simian sarcoma virus genome: demonstration that its  
A:Reference number: A03982; MUID:83144004

A:Accession: A01381  
A:Molecule type: genomic RNA  
A:Residues: 1-226 <DEV>  
C:Genetics:  
A:Gene: sis  
C:Superfamily: platelet-derived growth factor  
C:Keywords: growth factor; transforming protein  
F:6-226/Domain: platelet-derived growth factor chain B similarity <PDG>  
Query Match 13.8%; Score 104; DB 1; Length 226;  
Best Local Similarity 33.3%; Pred. No. 0.0073;  
Matches 36; Conservative 12; Mismatches 34; Indels 26; Gaps 9;  
QY 32 LTEVRLYSCTPRN--FSVSIREELKRTDTIF--WPGCLLVKRCGNCACCLHNCNECQC 87  
DB 73 VAEPAMIAECKTRTEVEFIS--RRLIDRTNANFLVMPVPCVEVRCSG---CC--NNRNVCQ 126  
QY 88 VPSKVTYKHYEVLQRLP-----KTGV---RGLHKSILTDVALEHHEECDC 128  
DB 127 RPTQV-----QLRPVQVRKIEIVRKPKIFKRAT-VTLEDHLACRC 165  
RESULT 14  
B49530  
vascular endothelial growth factor homolog A2R, 14.7K - Orf virus  
C:Species: Orf virus  
C:Date: 07-Apr-1994 #sequence\_revision 18-Nov-1994 #text\_change 08-Oct-1999  
C:Accession: B49530  
R:Lyttille, D.J.; Fraser, K.M.; Fleming, S.B.; Mercer, A.A.; Robinson, A.J.  
J. Virol. 68, 84-92, 1994  
A:Title: Homologs of vascular endothelial growth factor are encoded by the poxvirus o  
A:Reference number: A49530; MUID:94076465  
A:Contents: NZ2  
A:Accession: B49530  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-133 <LYT>  
A:CROSS-references: GB:S67520; NID:g456897; PIDN:AAB29220.1; PID:g456899  
A:Note: sequence inconsistent with nucleotide translation  
A:Note: sequence extracted from NCBI backbone (NCBIN:I41420, NCBI:P:141425)  
Query Match 13.6%; Score 102.5; DB 2; Length 133;  
Best Local Similarity 30.5%; Pred. No. 0.0063;  
Matches 32; Conservative 18; Mismatches 40; Indels 15; Gaps 6;  
QY 33 TEEVRLYSCTPRNFSVSIRE---ELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVCP 89  
DB 28 SEVLKGSECKPRPIVVPVSETHPEL--TSORFNPPCVTLMRCCG---CC--NDESLECV 80  
QY 90 SKVTYKHYEVLQRLPKTGVRGLHKSILTDVALEHHEECDCVCRGST 134  
DB 81 TEEVNTWELLG-ASGSGSNQMQR---LSFVEHKKKDCRPRFTT 120  
RESULT 15  
S52130  
vascular endothelial growth factor - pig  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 14-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 05-Nov-1999  
C:Accession: S52130  
R:Sharma, H.S.; Tang, Z.H.; Gho, B.C.G.; Verdouw, P.D.  
Biochim. Biophys. Acta 1260, 235-238, 1995  
A:Title: Nucleotide sequence and expression of the porcine vascular endothelial growt  
A:Reference number: S52130; MUID:95143284  
A:Accession: S52130  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-190 <SHA>  
A:CROSS-references: GB:X81380; NID:g587559; PIDN:CAA57143.1; PID:g587560

Query Match 13.6%; Score 102.5; DB 2; Length 190;  
Best Local Similarity 27.0%; Pred. No. 0.0087;  
Matches 24; Conservative 20; Mismatches 34; Indels 11; Gaps 4;  
QY 41 CTPRNFVSIREEL-KRTDTIFWPGCLLVKRCGGNACCLHNCNECQCVPKVKYHEV 99  
| | | | | : | | | | | : | | | | :  
Db 51 CRPIETLVDFQEPDEIEYIFKPSVFLMRCGG--CC--NDEGLECVPTTEFNITMQI 105  
| | | | | : | | | | | : | | | | :  
QY 100 LQLRPKTGVRGLIKSLTDVALEHHECDC 128  
: : : : | : : : : | : : : :  
Db 106 MRIKPHQG-----QHIGEMSFLOHNKCEC 129

Search completed: August 18, 2001, 01:52:09  
Job time: 925 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 18, 2001, 01:49:54 ; Search time 33.78 Seconds

(without alignments)

137.914 Million cell updates/sec

Title: US-09-457-066-2\_COPY\_210\_345

Perfect score: 754

Sequence: 1 LDLEDLYRPTWQLLKAFVF.....DVALEHHEECDCVCRGSTGG 136

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	114.5	15.2	148	1	VEGH_ORFN7
2	110	14.6	213	1	PDGA_RABIT
3	110	14.6	241	1	PDGB_HUMAN
4	108.5	14.4	164	1	VEGF_CAVPO
5	108	14.3	226	1	PDGA_XENLA
6	107	14.2	245	1	PDGB_FELCA
7	105.5	14.0	188	1	VEGB_HUMAN
8	104.5	13.9	215	1	VEGF_HUMAN
9	104	13.8	204	1	PDGA_RAT
10	104	13.8	211	1	PDGA_HUMAN
11	104	13.8	211	1	PDGA_MOUSE
12	104	13.8	226	1	TSIS_SMSAV
13	102.5	13.6	133	1	VEGH_ORFN2
14	102.5	13.6	190	1	VEGF_PIG
15	102.5	13.6	419	1	VEGC_HUMAN
16	101.5	13.5	146	1	VEGF_SHEEP
17	101.5	13.5	190	1	VEGF_BOVIN
18	101.5	13.5	415	1	VEGC_MOUSE
19	97	12.9	188	1	VEGB_MOUSE
20	96.5	12.8	190	1	VEGF_RAT
21	95.5	12.7	214	1	VEGF_MOUSE
22	94	12.5	225	1	PDGB_RAT
23	94	12.5	241	1	PDGB_MOUSE
24	90	11.9	241	1	PDGB_SHEEP
25	88.5	11.7	216	1	VEGF_CHICK
26	84	11.1	158	1	PLGF_MOUSE
27	83.5	11.1	5179	1	MUC2_HUMAN
28	79.5	10.5	170	1	PLGF_HUMAN
29	77.5	10.3	3672	1	LML2_CAEEL
30	73	9.7	60	1	MT_CHAC
31	73	9.7	60	1	MT_PAGBE
32	73	9.7	60	1	MT_PARCR
33	72	9.5	60	1	MT_DICLA

34	72	9.5	171	1	LMB1_HVDAT	Q27262 hydra atten
35	71.5	9.5	3712	1	LMA_DROME	Q00174 drosophila
36	71	9.4	60	1	MT_DROME	P52728 oreochromis
37	71	9.4	60	1	MT_ZOAVI	P52728 zoarcres viv
38	71	9.4	82	1	MT2B_LYCES	Q40158 lycopersico
39	71	9.4	767	1	MAO2_RICPR	O9zdf6 rickettsia
40	70.5	9.4	846	1	ITBX_DROME	P11584 drosophila
41	70	9.3	68	1	MT3_HORSE	P37360 equus cabal
42	70	9.3	68	1	MT3_PIG	P55944 sus scrofa
43	70	9.3	447	1	CLUS_RABIT	Q9xsc5 oryctolagus
44	69.5	9.2	445	1	CLUS_CANFA	P25473 canis famil
45	69	9.2	60	1	MT_LIZAU	O13257 liza aurata

#### ALIGNMENTS

RESULT 1  
VEGH\_ORFN7  
ID VEGH\_ORFN7 STANDARD; PRT; 148 AA.  
AC P52585;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE VASCULAR ENDOTHELIAL GROWTH FACTOR HOMOLOG PRECURSOR.  
GN A2R.  
OS Orf virus (strain NZ7) (OV NZ-7).  
OC Viruses: dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Parapoxvirus.  
OX NCBI\_TaxID=73495;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94076465; PubMed=8254780;  
RA Lytle D.J., Fraser K.M., Fleming S.B., Mercer A.A., Robinson A.J.;  
RT "Homologs of vascular endothelial growth factor are encoded by the  
poxvirus orf virus.";  
RL J. Virol. 68:84-92(1994).  
CC -!- FUNCTION: INDUCES ENDOTHELIAL PROLIFERATION.  
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.  
-----  
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or send an email to license@isb-sib.ch).  
-----  
CC EMBL; S67522; AAB29223.1;  
CC HSSP; P15692; 1VPE.  
DR InterPro: IPR000072;  
DR Pfam: PF00341; PDGF; 1.  
DR PROSITE; PS00249; PDGF\_1; FALSE\_NEG.  
DR PROSITE; PS50278; PDGF\_2; 1.  
KW Mitogen; Growth factor; Glycoprotein; Signal.  
FT SIGNAL 1 ?  
FT CHAIN ? 148  
FT VASCULAR ENDOTHELIAL GROWTH FACTOR  
FT HOMOLOG.  
FT DISULFID 46 88  
FT BY SIMILARITY.  
FT DISULFID 77 130  
FT BY SIMILARITY.  
FT DISULFID 81 132  
FT BY SIMILARITY.  
FT DISULFID 71 71  
FT INTERCHAIN (BY SIMILARITY).  
FT DISULFID 80 80  
FT INTERCHAIN (BY SIMILARITY).  
FT CARBOHYD 95 95  
FT N-LINKED (GLCNAC... ) (POTENTIAL).  
SQ SEQUENCE 148 AA; 16078 MW; F0E13BA104CC73F8 CRC64;

Query Match 15.2%; Score 114.5; DB 1; Length 148;  
Best Local Similarity 30.2%; Pred. No. 7.8e-05;  
Matches 29; Conservative 19; Mismatches 43; Indels 5; Gaps 3;  
Oy 41 CTPNFSVSIREEL-KRTDTIFWPGCLLVKRCGGNACCLHNCNECCQVPSVKYKHEV 99

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Db 46 CKPRDTVVYLGEEPESTNLQVNPCKVTKRCSG---CCNGDQICATAVETRTNTVTVSV 102
Qy 100 LQLRPKTVR-GLKSLKLDVALEHHEEDCVCRGSG 134
Db 103 TGVSSSGTSGNSTGNLQRLQISVTEHTKDCICIGRTTT 138

RESULT 2
PDGA_RABIT
ID PDGA_RABIT STANDARD; PRT; 213 AA.
AC P34007;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PLATELET-DERIVED GROWTH FACTOR, A CHAIN PRECURSOR (PDGF A-CHAIN)
DE (PDGF-1).
GN PDGFA.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-vascular smooth muscle;
RX MEDLINE=92246970; PubMed=1575749;
RA Nakahara K.-I., Nishimura H., Kuro O.M., Takewaki S.-I., Iwase M.,
RA Ohkubo A., Yazaki Y., Nagai R.;
RT "Identification of three types of PDGF-A chain gene transcripts in
RT rabbit vascular smooth muscle and their regulated expression during
RT development and by angiotensin II.";
RL Biochem. Biophys. Res. Commun. 184:811-818(1992).
CC -1- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR
CC CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS
CC AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS
CC RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE
CC IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEAL THE WOUND.
CC -1- SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A
CC AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN
CC TRANSFORMATION PROCESSES.
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; A1, A2 (SHOWN HERE) AND A3; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- INDUCTION: THE FORM A3 IS SELECTIVELY INDUCED BY ANGIOTENSIN II.
CC -1- MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE
CC PDGF RECEPTOR.
CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
DR PIR; JS0735; JS0735.
DR PIR; PS0387; PS0387.
DR PIR; JN0248; JN0248.
DR HSP; P01127; 1PDG.
DR InterPro; IPR000072; -.
DR InterPro; IPR002400; -.
DR Pfam; PF00341; PDGF; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS50278; PDGF_2; 1.
KW Glycoprotein; Mitogen; Growth factor; Platelet; Alternative splicing;
KW Signal.
FT SIGNAL.
FT 1 20
FT PROPEP 21 89
FT CHAIN 90 213
FT SITE 158 162
FT DISULFID 131 179
FT DISULFID 135 181
FT DISULFID 125 125
FT DISULFID 134 134
FT CARBOHYD 136 136
FT VARSPLIC 199 213
FT VARSPLIC 197 213
FT SEQUENCE 213 AA; 24005 MW; 28A9B7E50487F4C5 CRC64;

REMOVED BY PROTEOLYSIS (BY SIMILARITY).
PLATELET-DERIVED GROWTH FACTOR, A CHAIN.
RECEPTOR BINDING SITE (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
GRR -> DVR (IN ISOFORM A1).
MISSING (IN ISOFORM A1).
RRRESGKKRKRKRPT -> TLLPAPGVHPQCLRAHGD
COSRRNHQALGWRKKM (IN ISOFORM A3).
SEQUENCE 213 AA; 24005 MW; 28A9B7E50487F4C5 CRC64;

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Query Match 14.6%; Score 110; DB 1; Length 213;
Best Local Similarity 30.5%; Pred. No. 0.00032;
Matches 36; Conservative 16; Mismatches 48; Indels 18; Gaps 7;

Qy 22 RKSRRVDNLNLTTEVRLYSCTPRNFSVSI-REELKRTDTIF--WPGCLLYKRCGNCACC 78
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 85 RKRRTI-----EEAIPAICKRTVIYEIPRSQVDPTSAMFLIWPCCVEVKRCTG---CC 135
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 79 LHNCECQCVPKSVTKYKHEVLQLRPKTVGRLHKLKSLTDVALEHHEEDCVCRGSG 136
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 136 --NTSSVKQCPSPRV---HHRSVKVKVYVKKPK-LKEVQVRLHEHLEHCACAASSAG 187
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 3
PDGB_HUMAN
ID PDGB_HUMAN STANDARD; PRT; 241 AA.
AC P01127; P78431;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PLATELET-DERIVED GROWTH FACTOR, B CHAIN PRECURSOR (PDGF B-CHAIN)
DE (PDGF-2) (C-SIS) (BECAPLERMIN).
GN PDGFB OR SIS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84250325; PubMed=6740330;
RA Josephs S.F., Ratner L., Clarke M.F., Westin E.H., Reitz M.S.,
RA Wong-Staal F.;
RT "Transforming potential of human c-sis nucleotide sequences encoding
RT platelet-derived growth factor.";
RL Science 225:636-639(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86205961; PubMed=3517869;
RA Rao C.D., Igarashi H., Chiu I.-M., Robbins K.C., Aaronson S.A.;
RT "Structure and sequence of the human c-sis/platelet-derived growth
RT factor 2 (SIS/PDGF2) transcriptional unit.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2392-2396(1986).
RN [3]
RP SEQUENCE OF 22-241 FROM N.A.
RX MEDLINE=84205633; PubMed=6327048;
RA Chiu I.-M., Reddy E.P., Givol D., Robbins K.C., Tronick S.R.,
RA Aaronson S.A.;
RT "Nucleotide sequence analysis identifies the human c-sis
RT proto-oncogene as a structural gene for platelet-derived growth
RT factor.";
RL Cell 37:123-129(1984).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=85296313; PubMed=4033772;
RA Collins T., Ginsburg D., Boss J.M., Orkin S.H., Pober J.S.;
RT "Cultured human endothelial cells express platelet-derived growth
RT factor B chain: cDNA cloning and structural analysis.";
RL Nature 316:748-750(1985).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=85296623; PubMed=2991848;
RA Ratner L., Josephs S.F., Jarrett R., Reitz M.S., Wong-Staal F.;
RT "Nucleotide sequence of transforming human c-sis cDNA clones with
RT homology to platelet-derived growth factor.";
RL Nucleic Acids Res. 13:5007-5018(1985).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=87217119; PubMed=3472769;
RA Rao C.D., Igarashi H., Pech M.W., Robbins K.C., Aaronson S.A.;
RT "Oncogenic potential of the human platelet-derived growth factor
RT transcriptional unit.";
RL Cold Spring Harb. Symp. Quant. Biol. 51:959-966(1986).

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RN SEQUENCE FROM N.A.  
 RP Burgess J., Odell C.;  
 RA Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 RL [8]  
 RN SEQUENCE OF 1-53 FROM N.A.  
 RP MEDLINE=97141927; PubMed=8981877;  
 RA Simon M.-P., Pedoutour F., Sirvent N., Grosgeorge J., Minoletti F.,  
 RA Coindre J.-M., Terrier-Lacombe M.-J., Mandahl N., Craver R.D.,  
 RA Blin N., Sozzi G., Turc-Carel C., O'Brien K.P., Kedra D.,  
 RA Fransson I., Guilbaud C., Dumanaki J.P.;  
 RT "Deregulation of the platelet-derived growth factor B-chain gene via  
 RT fusion with collagen gene COL1A1 in dermatofibrosarcoma protuberans  
 RT and giant-cell fibroblastoma";  
 RL Nat. Genet. 15:95-98(1997).  
 [9]  
 RN SEQUENCE OF 26-241 FROM N.A.  
 RP MEDLINE=86164981; PubMed=3456904;  
 RA Weich H.A., Sebald W., Schairer H.U., Hoppe J.;  
 RT "The human osteosarcoma cell line U-2 OS expresses a 3.8 kilobase  
 RT mRNA which codes for the sequence of the PDGF-B chain";  
 RL FEBS Lett. 198:344-348(1986).  
 [10]  
 RN SEQUENCE OF 153-200 FROM N.A., AND PARTIAL SEQUENCE.  
 RP MEDLINE=84236121; PubMed=6329745;  
 RA Johnson A., Heldin C.H., Wasteson A., Westermark B., Deuel T.F.,  
 RA Huang J.S., Seeburg P.H., Gray A., Ullrich A., Scrae G.,  
 RA Stroobant P., Waterfield M.D.;  
 RT "The c-sis gene encodes a precursor of the B chain of  
 RT platelet-derived growth factor";  
 RL EMBO J. 3:921-928(1984).  
 [11]  
 RN SEQUENCE OF 82-110.  
 RP MEDLINE=83197379; PubMed=6844921;  
 RA Antoniadou H.N., Hunkapiller M.W.;  
 RT "Human platelet-derived growth factor (PDGF): amino-terminal amino  
 RT acid sequence";  
 RL Science 220:963-965(1983).  
 [12]  
 RN SEQUENCE OF 82-112.  
 RP MEDLINE=83244981; PubMed=6306471;  
 RA Waterfield M.D., Scrae G.T., Whittle N., Stroobant P., Johnson A.,  
 RA Wasteson A., Westermark B., Heldin C.H., Huang J.S., Deuel T.F.;  
 RT "Platelet-derived growth factor is structurally related to the  
 RT putative transforming protein p28sis of simian sarcoma virus";  
 RL Nature 304:35-39(1983).  
 [13]  
 RN MUTAGENESIS, & IMPORTANCE OF ARG-108 AND ILE-111 FOR RECEPTOR-BINDING.  
 RP MEDLINE=92097530; PubMed=1661670;  
 RA Clements J.M., Bawden L.J., Bloxidge R.E., Catlin G., Cook A.L.,  
 RA Craig S., Drummond A.H., Edwards R.M., Fallon A., Green D.R.,  
 RA Hellewell P.G., Kirwin P.M., Nayee P.D., Richardson S.J., Brown D.,  
 RA Chahwala S.B., Snarey M., Winslow D.;  
 RT "Two PDGF-B chain residues, arginine 27 and isoleucine 30, mediate  
 RT receptor binding and activation";  
 RL EMBO J. 10:4113-4120(1991).  
 [14]  
 RN INTERCHAIN DISULFIDE BONDS.  
 RP MEDLINE=92283833; PubMed=1317862;  
 RA Andersson M., Oestman A., Baekstrom G., Hellman U.,  
 RA George-Nascimento C., Westermark B., Heldin C.-H.;  
 RT "Assignment of interchain disulfide bonds in platelet-derived growth  
 RT factor (PDGF) and evidence for agonist activity of monomeric PDGF";  
 RL J. Biol. Chem. 267:11260-11266(1992).  
 [15]  
 RN X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).  
 RP MEDLINE=93010987; PubMed=1396586;  
 RA Oefner C., D'Arcy A., Winkler F.K., Eggmann B., Hosang M.;  
 RT "Crystal structure of human platelet-derived growth factor BB";  
 RL EMBO J. 11:3921-3926(1992).  
 CC -I- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR  
 CC CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS  
 CC AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS

CC RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE  
 CC IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEAL THE WOUND.  
 CC -I- SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A  
 CC AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN  
 CC TRANSFORMATION PROCESSES.  
 CC -I- PHARMACEUTICAL: AVAILABLE UNDER THE NAME REGRANEX (ORTHO-MCNEIL).  
 CC USED TO PROMOTE HEALING IN DIABETIC NEUROPATHIC FOOT ULCERS.  
 CC -I- MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE  
 CC PDGF RECEPTOR.  
 CC -I- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.  
 CC -I- DATABASE: NAME-R&D Systems' cytokine source book;  
 CC WWW="http://www.rndsystems.com/cyt\_cat/pdgf.html".  
 CC -I- DATABASE: NAME-Regranex; NOTE-Clinical information on Regranex;  
 CC WWW="http://www.regranex.com/".  
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 CC -----  
 DR EMBL; K01401; AAA60552.1;  
 DR EMBL; K01918; AAA60552.1; JOINED.  
 DR EMBL; J00121; AAA60552.1; JOINED.  
 DR EMBL; K01398; AAA60552.1; JOINED.  
 DR EMBL; K01399; AAA60552.1; JOINED.  
 DR EMBL; K01400; AAA60552.1; JOINED.  
 DR EMBL; X02811; CAA26579.1;  
 DR EMBL; M12783; AAA60553.1;  
 DR EMBL; X02744; CAA26524.1;  
 DR EMBL; K01917; AAA98793.1;  
 DR EMBL; K01913; AAA98793.1; JOINED.  
 DR EMBL; K01914; AAA98793.1; JOINED.  
 DR EMBL; K01915; AAA98793.1; JOINED.  
 DR EMBL; K01916; AAA98793.1; JOINED.  
 DR EMBL; X03702; CAA27333.1;  
 DR EMBL; Z81010; CAB02635.1;  
 DR EMBL; X00561; CAA25228.1;  
 DR EMBL; X00561; CAA25229.1;  
 DR EMBL; X98706; CAA67262.1;  
 DR PIR; A94276; PFHUG2.  
 DR PDB; 1PDG; 31-JAN-94.  
 DR MIM; 190040;  
 DR InterPro; IPR000072;  
 DR InterPro; IPR002400;  
 DR Pfam; PF00341; PDGF; 1.  
 DR PRINTS; PR00438; GFCYSKNOT.  
 DR PROSITE; PS00249; PDGF\_1; 1.  
 DR PROSITE; PS0278; PDGF\_2; 1.  
 KW Mitogen; Growth factor; Proto-oncogene; Platelet; Signal;  
 KW Pharmaceutical; 3D-structure.  
 FT SIGNAL 1 20  
 FT PROPEP 21 81  
 FT CHAIN 82 190  
 FT PROPEP 191 241  
 FT PROPEP 108 108  
 FT SITE 111 111  
 FT SITE 111 111  
 FT DISULFID 97 141  
 FT DISULFID 130 178  
 FT DISULFID 134 180  
 FT DISULFID 124 124  
 FT DISULFID 133 133  
 FT CONFLICT 21 21  
 FT CONFLICT 101 101  
 FT CONFLICT 105 105  
 FT CONFLICT 107 107  
 FT STRAND 90 91  
 FT STRAND 94 94  
 Query Match 14.6%; Score 110; DB 1; Length 241;  
 Best Local Similarity 32.9%; Pred. No. 0.00036;

PLATELET-DERIVED GROWTH FACTOR, B CHAIN.

INVOLVED IN RECEPTOR BINDING.  
INVOLVED IN RECEPTOR BINDING.INTERCHAIN.  
INTERCHAIN.E -> R (IN REF. 3).  
T -> E (IN REF. 11).  
E -> C (IN REF. 11).  
S -> C (IN REF. 11).



Matches 46; Conservative 13; Mismatches 37; Indels 44; Gaps 12;

Qy	2	DLEDLVRPTWQLLGKAFVFGKRSKVVNDLLT---EEVRLVSYCTPRN---FVSVIRELKKRT	57
Db	72	ELESRLAR-----GRRS-----LGSLTIAEPAMIAECKTRTEVEFIS--RRLIDRT	114
Qy	58	DTIF--WPGCLLVKRCGGNCACCLHNCNECQVPSVKTKYHEVLQLRP-----KTGV----	108
Db	115	NANFLVMPQCEVQRCSG---CC--NNRNVCQRPTQV-----QLRPVQVRKKEIVRK	161
Qy	109	RLGHKSITDVALEHHEECDC	128
Db	162	KPIFKKAT-VTLEDHLACK	180

RESULT	4
VEGF_CAVPO	
ID	VEGF_CAVPO
AC	STANDARD;
DT	PRT; 164 AA.
DT	P26617;
DT	01-AUG-1992 (Rel. 23, Created)
DT	01-AUG-1992 (Rel. 23, Last sequence update)
DT	01-OCT-1996 (Rel. 34, Last annotation update)
DE	VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VEF).
DE	GN VEGF.

OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata;  
 OC Mammalia; Eutheria; Rodentia;  
 RN NCBI\_TaxID=10141;  
 RP [1]  
 RP SEQUENCE FROM N.A.

RA Berse B.;  
RL Submitted (XX-1992) to the EMBL/GenBank/DBJ databases.  
CC  
CC !- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL  
CC CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR  
CC DEGENERABILITY

-1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.  
-1- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY SIMILARITY).

-- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS --

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CC	EMBL; M84230; AAA37057.1; -. BY SIMILARITY.
DR	HSP; P15692; 2VGH. BY SIMILARITY.
DR	IPRO; IPRO00072; -. BY SIMILARITY.
DR	Pfam; PF00341; PDGF_1. BY SIMILARITY.
DR	PROSITE; PS00249; PDGF_1; 1. INTERCHAIN (BY SIMILARITY).
DR	PROSITE; PS00278; PDGF_2; 1. INTERCHAIN (BY SIMILARITY).
KW	Mitogen; Growth factor; Glycoprotein. N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID 25 67 BY SIMILARITY.
FT	DISULFID 56 101 BY SIMILARITY.
FT	DISULFID 60 103 BY SIMILARITY.
FT	DISULFID 50 50 INTERCHAIN (BY SIMILARITY).
FT	DISULFID 59 59 INTERCHAIN (BY SIMILARITY).
FT	CARBOHYD 74 74
SQ	SEQUENCE 164 AA; 19330 MW; 9EB86A81A9D5DCA4 CRC64;

Query Match	14.4%	Score 108.5	DB 1	Length 164
Best Local Similarity	26.5%	Pred. No. 0.00035		
Matches 27	Conservative	21	Mismatches 37	Indels 17
			Gaps 5	

QY	34	EEVRLYS-----CTPRNFVSIREEL-KRTDIFWPGCLLVKRCGGNCACCLHNCNEQ	86
		:         :       :	
Db	12	EEVKFMDVYKRSRCPLEMLVDIFQEPDIEYIFKPSCVPLMKRCGG---CC--NDSLE	66

Qy 87 CVPSKVTKKYHEVLQLRPKTVGRGLHKSLTDVALEHHECDC 128  
 ||||: :|||:| : :||:| :||:|  
 Db 67 CVPTEENITQIMRIKPHQG----OHIGMSFLQHSKCEC 103

RESULT	5
PDGA_XENLA	
ID	PDGA_XENLA
STANDARD;	PRT; 226 AA.
AC	P13698;
DT	01-JAN-1990 (Rel. 13, Created)
DT	01-JAN-1990 (Rel. 13, Last sequence update)
DT	01-OCT-2000 (Rel. 40, Last annotation update)
DE	PLATELET-DERIVED GROWTH FACTOR, A CHAIN PRECURSOR (PDGF A-CHAIN)
DE	(PDGFA).

OS *Xenopus laevis* (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
 OC Xenopodinae; *Xenopus*.  
 NCBI\_TaxID=8355;  
 RN [1].

RP	SEQUENCE FROM N.A.
RC	TISSUE=Oocyte;
RX	MEDLINE=88321676; PubMed=3413486;

RA Mercola M., Melton D.A., Stiles C.D.;  
RT "platelet-derived growth factor A chain is maternally encoded in  
RT xenopus embryos.";  
RL Science 241:1223-1225(1988).

RN [2]  
RP SEQUENCE FROM N.A.

RC TISSUE=Oocyte;  
RX MEDLINE=90175018; PubMed=2308861;  
RA Bejcek B.E., Li D.Y., Deuel T.F.;

RT "Nucleotide sequence of a cDNA clone of *Xenopus* platelet-derived  
RT growth factor A-chain.";  
RL Nucleic Acids Res. 18:680-680(1990).

-1- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEAL THE WOUND.

-!- SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL A AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN TRANSFORMATION PROCESSES.

CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A  
CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. THE LONG FORM  
CC CONTAINS A BASIC INSERT WHICH ACTS AS A CELL RETENTION SIGNAL.

CC -|- MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE PDGF RECEPTOR.

CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS

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CC	-----
DR	EMBL; M23237; AAA49927.1; -
DR	EMBL; M23238; AAA49928.1; -
DR	EMBL; X17545; CAA35583.1; -
DR	PIR; S08220; S08220.
DR	HSSP; P01127; IPDG.

DR InterPro; IPR000072; -  
DR InterPro; IPR002400; -  
DR Pfam; PF00341; PDGF; 1.

DR PRINTS; PR00438; GFCYSKNOT.  
DR PROSITE; PS00249; PDGF\_1; 1.  
DR PROSITE; PS50278; PDGF\_2; 1.

KW	Glycoprotein; Mitogen; Growth factor; Platelet; Alternative splicing;
KW	Signal.
FT	SIGNAL 1 22

22

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or send an email to license@isb-sib.ch).
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EMBL: X05112; CAA28758.1; ALT_SEQ.
PIR: A26402; TVCTSS.
HSP: P01127; IPDG.
InterPro: IPR000072; -.
InterPro: IPR002400; -.
Pfam: PF00341; PDGF_1.
PRINTS: PR00438; GFCYSKNOT.
PROSITE: PS00249; PDGF_1; 1.
DR PROSITE; PS02078; PDGF_2; 1.
KW Mitogen; Growth factor; Proto-oncogene; Platelet; Signal.
FT SIGNAL 1 20
FT PROPEP 21 81
FT CHAIN 82 194
FT PROPEP 195 245
FT DISULFID 101 145
FT DISULFID 134 182
FT DISULFID 138 184
FT DISULFID 128 128
FT DISULFID 137 137
SQ SEQUENCE 245 AA; 27787 MW; E7715291D9837512 CRC64;

Query Match 14.2% Score 107; DB 1; Length 245;
Best Local Similarity 30.4%; Pred. No. 0.00074;
Matches 42; Conservative 15; Mismatches 45; Indels 36; Gaps 10;

QY 2 DLEDLYRPTWLLGKAFVGRKS--RVVDMLLTLTEEVRLYSCTPRN--FVSISIREELKRT 57
Db 72 ELESLSR-----GRRSLGEAAGSPVAEPAMIAECKRTTEVEFVS--RRLIDRT 118

QY 58 DTIF--WPGCLLYKRCGNACCLHNCOCVSKYTKKY-----HEVLQLRPKTGVRG 110
Db 119 NANELVMVPCVEVQRCSS--CC--NNRNVCQRTQQLRLVQVRKIEIVKRKP----- 167

QY 111 LHKSLTDVALEHHEECDC 128
Db 168 VFKKAT-VTLEDHLACKC 184

RESULT 7
VEGB_HUMAN STANDARD; PRT; 188 AA.
AC P49765;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED
DE FACTOR).
GN VEGFB OR VRF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96197355; PubMed=8637916;
RA Olofsson B., Pajusola K., Kaipainen A., von Euler G., Joukov V.,
RA Sakvela O., Orpana A., Pattersson R.F., Alitalo K., Eriksson U.;
RT "Vascular endothelial growth factor B, a novel growth factor for
RT endothelial cells.;"
RL Proc. Natl. Acad. Sci. U.S.A. 93:2576-2581(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97077124; PubMed=8919691;
RA Grimmond S., Lagercrantz J., Drinkwater C., Sillins G., Townson S.,
RA Pollock P., Gotley D., Carson E., Rakar S., Nordenskjold M., Ward L.,
RA Hayward N., Weber G.;
RT "Cloning and characterization of a novel human gene related to
RT vascular endothelial growth factor.;"

```

```
RL Genome Res. 6:124-131(1996).
CC -!- FUNCTION: GROWTH FACTOR FOR ENDOTHELIAL CELLS. BINDS HEPARIN.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED. CAN ALSO FORM HETERODIMER
CC WITH VEGF.
CC -!- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
CC TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXCEPT LIVER.
CC HIGHEST LEVELS FOUND IN HEART, SKELETAL MUSCLE AND PANCREAS.
CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U48801; AAB06274.1; -
DR EMBL: U43369; AAB91463.1; -
DR HSP: P15692; LVPP.
DR MIM: 601398; -
DR InterPro: IPR000072; -
DR Pfam: PF00341; PDGF_1;
DR PROSITE: PS00249; PDGF_1; 1.
DR PROSITE: PS0278; PDGF_2; 1.
KW Mitogen; Growth factor; Signal; Heparin-binding.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 188 VASCULAR ENDOTHELIAL GROWTH FACTOR B.
SQ SEQUENCE 188 AA; 21261 MW; F04654D5A3727194 CRC64;

Query Match 14.0%; Score 105.5; DB 1; Length 188;
Best Local Similarity 28.2%; Pred. No. 0.0008;
Matches 31; Conservative 22; Mismatches 40; Indels 17; Gaps 6;

QY 21 GRKSRVVD-LNLTVEVRLVSYCTPRNFSVSIREEELKRT-DTIFWPGCLLVKRGCGNACC 78
Db |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
30 GQRKVSQWIDYYTRA-----TCQPREVVPLTLMGTAKQLVPSCVTVQRCGG---CC 82
QY 79 LHCNCEQCVSPKTKYKHYEVLQRLPKTCVGLHKLSTDALEHHEECDC 128
Db |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
83 PD-DGLECVPTGQGRVQMILIRYPS-----SOLGEMSELEHSQCEC 124

RESULT 8
ID VEGF_HUMAN STANDARD; PRT; 215 AA.
AC P15692;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR
DE PERMEABILITY FACTOR) (VPF).
GN VEGF OR VEGFA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-90069608; PubMed=2479986;
RA Leung D.W., Cachianes G., Kuang W.-J., Goeddel D.V., Ferrara N.;
RT "Vascular endothelial growth factor is a secreted angiogenic
RT mitogen.";
RL Science 246:1306-1309(1989).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RA MEDLINE-90069609; PubMed=2479987;
RA Keck P.J., Hauser S.D., Krivi G., Sanzo K., Warren T., Feder J.,
RA Connolly D.T.;
RT "Vascular permeability factor, an endothelial cell mitogen related to
RT PDGF.";
CC
```

```
RL Science 246:1309-1312(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-91268072; PubMed=1711045;
RA Tischer E., Mitchell R., Hartman T., Silva M., Gospodarowicz D.,
RA Fiddes J.C., Abraham J.A.;
RT "The human gene for vascular endothelial growth factor. Multiple
RT protein forms are encoded through alternative exon splicing.";
RL J. Biol. Chem. 266:11947-11954(1991).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE-92231879; PubMed=1567395;
RA Weindel K., Marme D., Weich H.A.;
RT "Aids-associated Kaposi's sarcoma cells in culture express vascular
RT endothelial growth factor.";
RL Biochem. Biophys. Res. Commun. 183:1167-1174(1992).
RN [5]
RP PRELIMINARY SEQUENCE OF 27-36; 43-50 AND 59-81.
RX MEDLINE-90062112; PubMed=2584205;
RA Connolly D.T., Olander J.V., Heuvelman D., Nelson R., Monsell R.,
RA Siegel N., Haymore B.L., Leimgruber R., Feder J.;
RT "Human vascular permeability factor. Isolation from U937 cells.";
RL J. Biol. Chem. 264:20017-20024(1989).
RN [6]
RP SEQUENCE OF 27-41.
RX MEDLINE-93145946; PubMed=7678805;
RA Fleblich B.L., Jaeger B., Schoellmann C., Weindel K., Wiltling J.,
RA Kochs G., Marme D., Hug H., Weich H.A.;
RT "Synthesis and assembly of functionally active human vascular
RT endothelial growth factor homodimers in insect cells.";
RL Eur. J. Biochem. 211:19-26(1993).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 34-135.
RX MEDLINE-97352774; PubMed=9207067;
RA Muller Y.A., Li B., Christinger H.W., Wells J.A., Cunningham B.C.,
RA de Vos A.M.;
RT "Vascular endothelial growth factor: crystal structure and functional
RT mapping of the kinase domain receptor binding site.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:7192-7197(1997).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (1.93 ANGSTROMS) OF 34-135.
RX MEDLINE-98035455; PubMed=9351807;
RA Muller Y.A., Christinger H.W., Keyt B.A., de Vos A.M.;
RT "The crystal structure of vascular endothelial growth factor (VEGF)
RT refined to 1.93-A resolution: multiple copy flexibility and receptor
RT binding.";
RL Structure 5:1325-1338(1997).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 39-134.
RX MEDLINE-99119204; PubMed=9922142;
RA Wiesmann C., Christinger H.W., Cochran A.G., Cunningham B.C.,
RA Fairbrother W.J., Keenan C.J., Meng G., de Vos A.M.;
RT "Crystal structure of the complex between VEGF and a receptor-blocking
RT peptide.";
RL Biochemistry 37:17765-17772(1998).
RN [10]
RP STRUCTURE BY NMR OF 34-135.
RX MEDLINE-9747915; PubMed=9336848;
RA Fairbrother W.J., Champe M.A., Christinger H.W., Keyt B.A.,
RA Starovasnik M.A.;
RT "1H, 13C, and 15N backbone assignment and secondary structure of the
RT receptor-binding domain of vascular endothelial growth factor.";
RL Protein Sci. 6:2250-2260(1997).
RN [11]
RP STRUCTURE BY NMR OF 137-215.
RX MEDLINE-98298440; PubMed=9634701;
RA Fairbrother W.J., Champe M.A., Christinger H.W., Keyt B.A.,
RA Starovasnik M.A.;
RT "Solution structure of the heparin-binding domain of vascular
RT endothelial growth factor.";
RL Structure 6:637-648(1998).
RN [12]
RP -!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL
CC CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR
```



[illegible]

different precursor proteins.";  
Mol. Cell. Biol. 8:571-577(1988).  
[3]  
SEQUENCE FROM N.A.  
MEDLINE=86203630; PubMed=3754619;  
Bethsholtz C., Johansson A., Heldin C.H., Westermark B., Lind P.,  
Urdea M.S., Eddy R., Shows T.B., Philpott K., Mellor A.L., Knott T.J.,  
Scott J.;  
"cDNA sequence and chromosomal localization of human platelet-derived  
growth factor A-chain and its expression in tumour cell lines.";  
Nature 320:695-699(1986).  
[4]  
SEQUENCE FROM N.A.  
MEDLINE=88030061; PubMed=3666150;  
Hoppe J., Schumacher L., Eichner W., Welch H.A.;  
"The long 3'-untranslated regions of the PDGF-A and -B mRNAs are only  
distantly related.";  
FEBS Lett. 223:243-246(1987).  
[5]  
SEQUENCE OF 1-53 FROM N.A.  
MEDLINE=93252628; PubMed=8486521;  
Takimoto Y., Li W.Y., Wang Z.Y., Tong B.D., Deuel T.F.;  
"Nucleotide sequence of the 5' region of the human platelet-derived  
growth factor A-chain gene.";  
Hiroshima J. Med. Sci. 42:47-52(1993).  
[6]  
ALTERNATIVE SPLICING.  
MEDLINE=87287247; PubMed=3614363;  
Tong B.D., Auer D.E., Jaye M., Kaplow J.M., Ricca G., McConathy E.,  
Drohan W., Deuel T.F.;  
"cDNA clones reveal differences between human glial and endothelial  
cell platelet-derived growth factor A-chains.";  
Nature 328:619-621(1987).  
[7]  
ALTERNATIVE SPLICING.  
MEDLINE=87287248; PubMed=3614364;  
Collins T., Bonthron D.T., Orkin S.H.;  
"Alternative RNA splicing affects function of encoded platelet-derived  
growth factor A chain.";  
Nature 328:621-624(1987).  
[8]  
INTERCHAIN DISULFIDE BONDS.  
MEDLINE=92283833; PubMed=1317862;  
Andersson M., Oestman A., Baeckstrom G., Hellman U.,  
George-Nascimento C., Westermark B., Heldin C.-H.;  
"Assignment of interchain disulfide bonds in platelet-derived growth  
factor (PDGF) and evidence for agonist activity of monomeric PDGF.";  
J. Biol. Chem. 267:11260-11266(1992).  
CC -!- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR  
CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS  
AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS  
RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE  
IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEAL THE WOUND.  
CC -!- SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A  
AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN  
TRANSFORMATION PROCESSES.  
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A  
SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. THE LONG FORM  
CONTAINS A BASIC INSERT WHICH ACTS AS A CELL RETENTION SIGNAL.  
CC -!- MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE  
PDGF RECEPTOR.  
CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.  
CC -!- DATABASE: NAME=R&D Systems' cytokine source book;  
WWW="http://www.rndsystems.com/cyt\_cat/pdgrf.html".  
-----  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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DR EMBL; M21571; -; NOT_ANNOTATED_CDS.
DR EMBL; X03795; CAA27421.1; -
DR EMBL; X06374; CAA29677.1; -
DR EMBL; M20494; AAA60045.1; JOINED.
DR EMBL; M20488; AAA60045.1; JOINED.
DR EMBL; M20489; AAA60045.1; JOINED.
DR EMBL; M20490; AAA60045.1; JOINED.
DR EMBL; M20491; AAA60045.1; JOINED.
DR EMBL; M20492; AAA60045.1; JOINED.
DR EMBL; M20493; AAA60045.1; JOINED.
DR EMBL; M19988; AAA60046.1; -
DR EMBL; M21571; AAA60046.1; JOINED.
DR EMBL; M19984; AAA60046.1; JOINED.
DR EMBL; M19985; AAA60046.1; JOINED.
DR EMBL; M19986; AAA60046.1; JOINED.
DR EMBL; M19987; AAA60046.1; JOINED.
DR EMBL; M19989; AAA60047.1; -
DR EMBL; M21571; AAA60047.1; JOINED.
DR EMBL; M19984; AAA60047.1; JOINED.
DR EMBL; M19985; AAA60047.1; JOINED.
DR EMBL; M19986; AAA60047.1; JOINED.
DR EMBL; M19987; AAA60047.1; JOINED.
DR EMBL; A09204; CAA00830.1; -
DR EMBL; S62078; AAB26566.1; -
DR PIR; A28964; PFHUG1.
DR PIR; B28964; B28964.
DR HSSP; P01127; 1PDG.
DR MIM; I73430; -
DR InterPro; IPR000072; -
DR InterPro; IPR002400; -
DR Pfam; PF00341; PDGF; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
KW Glycoprotein; Mitogen; Growth factor; Platelet; Alternative splicing;
KW Signal.
FT SIGNAL. 1 20
FT PROPEP 21 86
FT CHAIN 87 211
FT SITE 158 162
FT DISULFID 96 140
FT DISULFID 129 177
FT DISULFID 133 179
FT DISULFID 123 123
FT DISULFID 132 132
FT CARBOHYD 134 134
FT VARSPIC 194 196
FT VARSPIC 197 211
FT CONFLICT 64 66
FT SEQUENCE 211 AA; 24043 MW; 48633DDE558EFA43 CRC64;

Query Match 13.88; Score 104; DB 1; Length 211;
Best Local Similarity 34.08; Pred. No. 0.0013;
Matches 32; Conservative 12; Mismatches 34; Indels 16; Gaps 6;

QY 41 CTRNFTSVSI-REELKRTDIF--WPGCLLVKRCGGNCACCLHNCNQCQVPSKV---TK 94
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| : : : : : | : : : : | : : : : | : : : : |
QY 95 KYHEVLQLRPKTGVRGLHKSITDVALEHHERCDC 128
| : : : : : | : : : : | : : : : | : : : : |
Db 151 KVAKVEVVRKPKLKEV-----QVRLEHLEAC 179
| : : : : : | : : : : | : : : : | : : : : |

RESULT 11
PDGA_MOUSE
ID PDGA_MOUSE STANDARD; PRT; 211 AA.
AC P20033;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PLATELET-DERIVED GROWTH FACTOR, A CHAIN PRECURSOR (PDGF A-CHAIN)

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DE (PDGF-1).
GN PDGFA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (LONG AND SHORT FORMS).
RC STRAIN=BALB/C;
RX MEDLINE=94031105; PubMed=1340209;
RA Rorsman F., Betsholtz C.;
RT "Characterization of the mouse PDGF A-chain gene. Evolutionary
RT conservation of gene structure, nucleotide sequence and alternative
RT splicing.";
RL Growth Factors 6:303-313(1992).
RN [2]
RP SEQUENCE FROM N.A. (SHORT FORM).
RC STRAIN=F9;
RX MEDLINE=90169294; PubMed=2155144;
RA Mercola M., Wang C., Kelly J., Brownlee C., Jackson-Grusby L.,
RA Stiles C., Bowen-Pope D.;
RT "Selective expression of PDGF A and its receptor during early mouse
RT embryogenesis.";
RL Dev. Biol. 138:114-122(1990).
CC -!- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR
CC CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS
CC AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS
CC RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE
CC IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEALS THE WOUND.
CC -!- SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A
CC AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN
CC TRANSFORMATION PROCESSES.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. THE LONG FORM
CC CONTAINS A BASIC INSERT WHICH ACTS AS A CELL RETENTION SIGNAL.
CC -!- MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE
CC PDGF RECEPTOR.
CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC
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CC
DR EMBL; S66873; AAB28740.2; -
DR EMBL; S66868; AAB28740.2; JOINED.
DR EMBL; S66869; AAB28740.2; JOINED.
DR EMBL; S66870; AAB28740.2; JOINED.
DR EMBL; S66871; AAB28740.2; JOINED.
DR EMBL; S66872; AAB28740.2; JOINED.
DR EMBL; S66874; AAB28741.2; -
DR EMBL; S66868; AAB28741.2; JOINED.
DR EMBL; S66869; AAB28741.2; JOINED.
DR EMBL; S66870; AAB28741.2; JOINED.
DR EMBL; S66871; AAB28741.2; JOINED.
DR EMBL; S66872; AAB28741.2; JOINED.
DR EMBL; M29464; AAA39903.1; -
DR PIR; A37359; A37359.
DR HSSP; P01127; 1PDG.
DR MGD; MGI:97527; pdgfa.
DR InterPro; IPR000072; -
DR InterPro; IPR002400; -
DR Pfam; PF00341; PDGF; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
KW Glycoprotein; Mitogen; Growth factor; Platelet; Alternative splicing;
KW Signal.
FT SIGNAL. 1 20
FT PROPEP 21 86
FT SEQUENCE 211 AA; 24043 MW; 48633DDE558EFA43 CRC64;

```

REMOVED BY PROTEOLYSIS.



VEGC\_HUMAN STANDARD; PRT; 419 AA.

AC P49767;

AD 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR (VEGF-C) (VASCULAR

DE ENDOTHELIAL GROWTH FACTOR RELATED PROTEIN) (VRP) (FLT4 LIGAND) (FLT4-

DE L).

GN VEGFC.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI\_TaxID=9606;

[1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 103-120.

RX MEDLINE=96178224; PubMed=8617204;

RA Joukov V., Pajusola K., Kaipainen A., Chilov D., Lahtinen I., Kukk E.,

RA Saksa O., Kalkkinen N., Alitalo K.;

RT "A novel vascular endothelial growth factor, VEGF-C, is a ligand for

RT the Flt4 (VEGFR-3) and KDR (VEGFR-2) receptor tyrosine kinases.;"

RL EMBO J. 15:290-298(1996).

[2]

RP ERRATUM.

RX MEDLINE=96203094; PubMed=8612600;

RA Joukov V., Pajusola K., Kaipainen A., Chilov D., Lahtinen I., Kukk E.,

RA Saksa O., Kalkkinen N., Alitalo K.;

RL EMBO J. 15:1751-1751(1996).

[3]

RP SEQUENCE FROM N.A.

RX MEDLINE=96312526; PubMed=8700872;

RA Lee J., Gray A., Yuan J., Luch S.-M., Avraham H., Wood W.I.;

RT "Vascular endothelial growth factor-related protein: a ligand and

RT specific activator of the tyrosine kinase receptor Flt4.;"

RL Proc. Natl. Acad. Sci. U.S.A. 93:1988-1992(1996).

[4]

RP SEQUENCE FROM N.A.

RA Fitz L., Morris J.C., Towler P.S., Long A.J., Greco R.,

RA Burgess P., Giannotti J., Clarietta A., Hennessey D., Kovacic S.,

RA Fitzgerald M., Scaltreto H., Welch N., Neben S., Finnerty H.,

RA Zollner R., Wang J., Nickbarg E., Gassaway R., Turner K.,

RA Wood C.R.;

RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL

CC CELL GROWTH.

CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.

CC -1- PTM: PROBABLY PROTEOLITICALLY PROCESSED IN THE C-TERMINUS.

CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.

CC

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC

DR EMBL; X94216; CAA63907.1; -;

DR EMBL; U43142; AAA85214.1; -;

DR EMBL; U58111; AAA02909.1; -;

DR HSSP; P15692; 1VPF.

DR MIM; 601528; -;

DR InterPro; IPR000072; -;

DR InterPro; IPR002400; -;

DR Pfam; PF00341; PDGF; 1.

DR PRINTS; PR00438; GFCYSKNOT.

DR PROSITE; PS00249; PDGF.1; 1.

DR PROSITE; PS0278; PDGF.2; 1.

KW Mitogen; Growth factor; Glycoprotein; Signal; Repeat.

FT SIGNAL 1 ?

FT PROPEP ? 102

FT CHAIN 103 419

FT DOMAIN 275 365

FT 4 X 24 AA TANDEM REPEATS.

```

RESULT 14
VEGF_PIG STANDARD; PRT; 190 AA.
ID VEGF_PIG AC P49151;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPF).
DN VEGF.
GN VEGF.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
[1]
SEQUENCE FROM N.A.
RP TISSUE=Heart;
RX MEDLINE=95143284; PubMed=7841203;
RA Sharma H.S., Tang Z.H., Gho B.C.H., Verdouw P.D.;
RT "Nucleotide sequence and expression of the porcine vascular endothelial growth factor.";
RL Biochim. Biophys. Acta 1260:235-238(1995).
CC -I- CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR PERMEABILITY (BY SIMILARITY).
CC CC CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR PERMEABILITY (BY SIMILARITY).
CC CC -I- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC CC -I- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY SIMILARITY).
CC CC -I- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
-----
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EMBL; X81380; CAA57143.1; .
DR HSSP; P15692; 2VGH.
DR InterPro; IPR000072; .
DR Pfam; PF00341; PDGF_1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
KW Mitogen; Growth factor; Glycoprotein; Signal.
FT SIGNAL
FT CHAIN 26 POTENTIAL.
FT CHAIN 27 190 VASCULAR ENDOTHELIAL GROWTH FACTOR.
FT DISULFID 51 93 BY SIMILARITY.
FT DISULFID 82 127 BY SIMILARITY.
FT DISULFID 86 129 BY SIMILARITY.
FT DISULFID 76 76 INTERCHAIN (BY SIMILARITY).
FT DISULFID 85 85 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 100 100 N-LINKED (GLCNAC.. ) (POTENTIAL).
SQ SEQUENCE 190 AA; 22368 MW; 04D40B8D7913047F CRC64;

Query Match 13.6%; Score 102.5; DB 1; Length 190;
Best Local Similarity 27.0%; Pred. No. 0.0016;
Matches 24; Conservative 20; Mismatches 34; Indels 11; Gaps 4;

QY 41 CTPRNFVSIVREEL-KRTDTIFPGCLLVKRGCGNCACLLHCNCOCVPSKYTKYHEV 99
DB 51 CRPIETVLDFIQEYPDDIEYIFKPSCVPLMKRCGG--CC--NDEGLECVPEEFNTMQI 105

QY 100 LQLRPKTGVRGLKSLTDVALEHHECDC 128
DB 106 MRIPKHOG----QHIGEMSFLQHNKCEC 129

RESULT 15
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FT REPEAT 275 298 1.
FT REPEAT 299 322 2.
FT REPEAT 323 346 3.
FT REPEAT 347 365 4 (PARTIAL).
FT CARBOHYD 175 175 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 240 240 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 419 AA; 46883 MW; 9F598719DB3E014F CRC64;

Query Match 13.6%; Score 102.5; DB 1; Length 419;
Best Local Similarity 28.2%; Pred No. 0.0036;
Matches 31; Conservative 15; Mismatches 43; Indels 21; Gaps 6;

Qy 29 LNLTEEVRLYSCTPRNFVSIREEL-KRTDTIFWPGCLLVKRCGNCACCLHNCNECQC 87
Db 119 LKSIDNEWKTCQMPREVCIDVGKEFGVATNFFKPPCVSVYRCGG---CC--NSEGLQC 173

Qy 88 V---PSKYTKKYHEV---LQLRPKTGVRGLHKS LTDVALEHHEEDCVCR 131
Db 174 MNTSTSYLSKTLFEITVPLSQGPKP-----VTISFANHNTSCRCMSK 214
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Search completed: August 18, 2001, 01:54:44  
Job time: 290 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 18, 2001, 01:48:14 ; Search time 98.1 Seconds  
(without alignments)  
183.420 Million cell updates/sec

Title: US-09-457-066-2\_COPY\_210\_345  
Perfect score: 754  
Sequence: 1 LDLEDLRPTWQLLKARVF.....DVALEHHREDCVCRGSTGG 136

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL16:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mnc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_unclassified:\*  
13: sp\_vertebrate:\*  
14: sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	754	100.0	345	4 Q9UL22	Q9ul22 homo sapien
2	754	100.0	345	4 Q9NRA1	Q9nra1 homo sapien
3	697	92.4	345	11 Q9QY71	Q9qy71 mus musculus
4	681	90.3	345	11 Q9JHV8	Q9jvh8 mus musculus
5	679	90.1	345	11 Q9EQX6	Q9eqx6 rattus norv
6	673	89.3	345	13 Q91946	Q91946 gallus gall
7	346.5	46.0	370	11 Q9BQT1	Q9eqt1 rattus norv
8	344.5	45.7	370	4 Q9GZP0	Q9gzp0 homo sapien
9	121.5	16.1	326	11 Q35251	Q35251 rattus norv
10	119.5	15.8	358	11 P97946	P97946 mus musculus
11	117	15.5	148	13 Q42571	Q42571 xenopus lae
12	117	15.5	194	13 Q42572	Q42572 xenopus lae
13	116	15.4	354	4 Q43915	Q43915 homo sapien
14	110	14.6	185	4 Q15354	Q15354 homo sapien
15	110	14.6	226	4 Q9UF23	Q9uf23 homo sapien
16	107	14.2	210	6 Q29613	Q29613 felis silve
17	105.5	14.0	207	4 Q16528	Q16528 homo sapien
18	104.5	13.9	147	4 Q9UH58	Q9uh58 homo sapien
19	104.5	13.9	171	4 Q9H1W8	Q9h1w8 homo sapien

Query Match 100.0% Score 754; DB 4; Length 345;

20	104.5	13.9	174	4 Q9UL23	Q9ul23 homo sapien
21	104.5	13.9	209	4 Q60720	Q60720 homo sapien
22	104.5	13.9	232	4 Q9H1W9	Q9h1w9 homo sapien
23	104.5	13.9	254	4 Q16889	Q16889 homo sapien
24	102.5	13.6	190	6 Q9XSF3	Q9xsf3 canis famil
25	102.5	13.6	190	6 Q9GL52	Q9gl52 sus scrofa
26	102.5	13.6	208	6 Q9XSF4	Q9xsf4 canis famil
27	102.5	13.6	214	6 Q9XSF5	Q9xsf5 canis famil
28	102.5	13.6	214	6 Q9MYV3	Q9myv3 canis famil
29	102	13.5	188	6 Q9XS48	Q9xs48 bos taurus
30	102	13.5	193	6 Q9XS49	Q9xs49 bos taurus
31	102	13.5	301	5 Q9WVP6	Q9wvp6 drosophila
32	101.5	13.5	118	6 Q9WZB1	Q9wzb1 ovis aries
33	101.5	13.5	124	6 Q9CK00	Q9ck00 callithrix
34	101.5	13.5	190	6 Q77643	Q77643 ovis aries
35	101.5	13.5	418	13 Q57352	Q57352 coturnix co
36	101.5	13.5	420	6 Q9XS50	Q9xs50 bos taurus
37	100.5	13.3	144	13 Q73822	Q73822 brachydanio
38	100.5	13.3	188	13 Q73682	Q73682 brachydanio
39	100.5	13.3	190	11 Q9QX39	Q9qx39 spalax leuc
40	98	13.0	75	6 Q18843	Q18843 oryctolagus
41	98	13.0	78	6 Q9N1S2	Q9n1s2 capreolus c
42	98	13.0	123	6 Q9N1S1	Q9n1s1 capreolus c
43	98	13.0	211	13 Q9PUF7	Q9puf7 gallus gall
44	97.5	12.9	146	11 Q9QXG6	Q9qxg6 rattus norv
45	97.5	12.9	190	6 Q9GKR0	Q9gkr0 equus cabal

ALIGNMENTS

RESULT 1  
Q9UL22  
ID Q9UL22 PRELIMINARY; PRT; 345 AA.  
AC Q9UL22;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE SECRETORY GROWTH FACTOR-LIKE PROTEIN FALLOTEIN (SPINAL CORD-DERIVED GROWTH FACTOR).  
GN HSCDGF.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=UTERUS;  
RA Tsai Y.J., Lee R.K.K., Lin S.P.;  
RT "Falloletin, a novel growth factor like gene identified in human uterus."  
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN;  
RX MEDLINE=20317014; PubMed=10858496;  
RA Hanada T., Ui-Tei K., Miyata Y.;  
RT "A novel gene derived from developing spinal cords, SCDGF, is a unique member of the PDGF/VEGF family."  
RL FEBS Lett. 475:97-102(2000).  
DR EMBL; AF091434; AAF00049.1; -  
DR EMBL; AB033831; BAB03266.1; -  
DR InterPro; IPR000072; -  
DR InterPro; IPR000859; -  
DR Pfam; PF00341; PDGF; 1.  
DR Pfam; PF00431; CUB; 1.  
DR PROSITE; PS01180; CUB; 1.  
DR PROSITE; PS50278; PDGF\_2; 1.  
DR SMART; SM00042; CUB; 1.  
SQ SEQUENCE 345 AA; 39029 MW; CDE9E51F40633E78 CRC64;

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Best Local Similarity 100.0%; Pred. No. 3.le-75;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDLEDLYRPTWQLLGKAFVFGKRSRVVDNLNLTTEEVRLYSCTPRNFSVIREELKRTDTI 60
DB 210 LDLEDLYRPTWQLLGKAFVFGKRSRVVDNLNLTTEEVRLYSCTPRNFSVIREELKRTDTI 269

QY 61 FWPGLLVKRCGGNACCLHNCNECCQVPSKVKYKHYEVLQRPKTGVRLHKSLLTDVAL 120
DB 270 FWPGLLVKRCGGNACCLHNCNECCQVPSKVKYKHYEVLQRPKTGVRLHKSLLTDVAL 329

QY 121 EHHECDVCVRGSGTG 136
DB 330 EHHECDVCVRGSGTG 345

RESULT 2
Q9NRAL ID Q9NRAL PRELIMINARY; PRT; 345 AA.
AC Q9NRAL;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE PLATELET-DERIVED GROWTH FACTOR C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Li X., Ponten A., Aase K., Karlsson L., Abramson A., Uutela M.,
RA Backstrom G., Hellstrom M., Bostrom H., Li H., Soriano P.,
RA Batscholtz C., Heldin C.-H., Alitalo K., Ostman A., Eriksson U.;
RT "PDGF-C is a novel protease-activated ligand for the PDGF alpha
RT receptor.";
RL Nat. Cell Biol. 0:0-0(2000).
DR EMBL; AF244813; AAF80597.1; -
DR InterPro; IPR000072; -
DR InterPro; IPR000859; -
DR Pfam; PF00341; PDGF_1;
DR Pfam; PF00431; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF_2; 1.
DR SMART; SM00042; CUB; 1.
SQ SEQUENCE 345 AA; 39043 MW; 590889CEA55CC5EA CRC64;

Query Match 100.0%; Score 754; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 3.le-75;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDLEDLYRPTWQLLGKAFVFGKRSRVVDNLNLTTEEVRLYSCTPRNFSVIREELKRTDTI 60
DB 210 LDLEDLYRPTWQLLGKAFVFGKRSRVVDNLNLTTEEVRLYSCTPRNFSVIREELKRTDTI 269

QY 61 FWPGLLVKRCGGNACCLHNCNECCQVPSKVKYKHYEVLQRPKTGVRLHKSLLTDVAL 120
DB 270 FWPGLLVKRCGGNACCLHNCNECCQVPSKVKYKHYEVLQRPKTGVRLHKSLLTDVAL 329

QY 121 EHHECDVCVRGSGTG 136
DB 330 EHHECDVCVRGSGTG 345

RESULT 3
Q9QY71 ID Q9QY71 PRELIMINARY; PRT; 345 AA.
AC Q9QY71;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE FALLOTEIN.

Best Local Similarity 100.0%; Pred. No. 3.le-75;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDLEDLYRPTWQLLGKAFVFGKRSRVVDNLNLTTEEVRLYSCTPRNFSVIREELKRTDTI 60
DB 210 LDLEDLYRPTWQLLGKAFVFGKRSRVVDNLNLTTEEVRLYSCTPRNFSVIREELKRTDTI 269

QY 61 FWPGLLVKRCGGNACCLHNCNECCQVPSKVKYKHYEVLQRPKTGVRLHKSLLTDVAL 120
DB 270 FWPGLLVKRCGGNACCLHNCNECCQVPSKVKYKHYEVLQRPKTGVRLHKSLLTDVAL 329

QY 121 EHHECDVCVRGSGTG 136
DB 330 EHHECDVCVRGSGTG 345

RESULT 4
Q9JHV8 ID Q9JHV8 PRELIMINARY; PRT; 345 AA.
AC Q9JHV8;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE PLATELET-DERIVED GROWTH FACTOR C.
GN PDGFC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SWISS-WEBSTER/NIH;
RA Ding H., Wu X., Kim I., Tam P.P.L., Koh G.Y., Nagy A.;
RT "The mouse pdgfc gene: Dynamic expression in embryonic tissues during
RT organogenesis.";
RL Mech. Dev. 0:0-0(2000).
DR EMBL; AF286725; AAF91483.1; -
DR InterPro; IPR000072; -
DR InterPro; IPR000859; -
DR Pfam; PF00431; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF_2; 1.
DR SMART; SM00042; CUB; 1.
SQ SEQUENCE 345 AA; 38866 MW; FA1486BED6D362F8 CRC64;

Query Match 90.3%; Score 681; DB 11; Length 345;
Best Local Similarity 87.5%; Pred. No. 3.6e-67;
Matches 119; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 1 LDLEDLYRPTWQLLGKAFVFGKRSRVVDNLNLTTEEVRLYSCTPRNFSVIREELKRTDTI 60
DB 210 LDLEDLYRPTWQLLGKAFVFGKRSRVVDNLNLTTEEVRLYSCTPRNFSVIREELKRTDTI 269
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DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE	SPINAL CORD-DERIVED GROWTH FACTOR-B (MSTP036).
GN	HSCDGF-B.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RN	SEQUENCE FROM N.A.
RP	Hanada T., Ui-Tai K., Imaki J., Miyata Y.;
RA	"Molecular Cloning of SCDFG-B, a Novel Growth Factor Homologous to
RT	SCDFG/PDGF-C/fallotenein."
RL	Biochem. Biophys. Res. Commun. 0:0-0(2000).
RZ	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=AORTA;
RA	Liu B., Liu Y.Q., Wang X.Y., Zhao B., Sheng H., Zhao X.W., Liu S.,
RA	Xu Y.Y., Ye J., Song L., Gao Y., Zhang C.L., Zhang J., Wei Y.J.,
RA	Cao H.Q., Zhao Y., Liu L.S., Ding J.F., Gao R.L., Wu Q.Y., Qiang B.O.,
RA	Yuan J.G., Liew C.C., Zhao M.S., Hui R.T.;
RL	Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AB03832; BABI8903.1; -
DR	EMBL; AF113216; AAG39287.1; -
SQ	SEQUENCE 370 AA; 42848 MW; D387F485E7BB7674 CRC64;
Query Match	45.7%; Score 344.5; DB 4; Length 370;
Best Local Similarity	50.0%; Pred. No. 5.4e-30;
Matches 66; Conservative 21; Mismatches 40; Indels 5; Gaps	
QY	2 DLELYRPTWOLGLKAFVGRKSRVDNLNLTTEVRLYSCTPRNFVSIREELKRTDTIF 61       : : : :       : : : :       : : : :       : : : :       : : : :
Db	235 DLENWLDTPRYGRSY-HDRKK-VOLDRLNDARKYSCTPRNYSVNREELKANVF 292
QY	62 WPGCLLVKRGCGNACCLHNCNECQCVPKVKTKYHEVLQLRP---KTGVYRGLHKSLTDV 118 :       :       :           :       :           :           :           :
Db	293 FPRCLLVQRGGNGCGTWNWSCTCNCSGTAKVKKYHEVLQFEPGHKRRGRAKTMALVDI 352
QY	119 ALEHHRECDCVC 130   :             :
Db	353 OLDHHERCDCIC 364
RESULT 9	
O35251	PRELIMINARY; PRT; 326 AA.
ID O35251	
AC O35251;	
DT 01-JAN-1998 (TrEMBLrel. 05, Created)	
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)	
DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)	
DE VASCULAR ENDOTHELIAL GROWTH FACTOR D.	
GN VEGF-D.	
OS Rattus norvegicus (Rat).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
OX NCBI_TaxID=10116;	
RN [1]	
RN SEQUENCE FROM N.A.	
RC STRAIN=SPRAGUE DAWLEY;	
RX MEDLINE=97349118; PubMed=9205122;	
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DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
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GN VEGF.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
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RA Cleaver O., Tonissen K.F., Saha M.S., Krieg P.A.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
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DR HSSP; P15692; 1VPP.
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OY 118 VALEHHEECDC 128
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DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE GROWTH FACTOR FIGF.
GN FIGF OR VEGF-D.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
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RP SEQUENCE FROM N.A.
RA MEDLINE=98140120; PubMed=9479493;
RA Rocchigiani M., Lestingi M., Luddi A., Orlandini M., Franco B.,
RA Rossi E., Ballabio A., Zuffardi O., Oliviero S.;
RT "Human FIGF: cloning, gene structure, and mapping to chromosome Xp22.1
RT between the FIGA and the GRPR genes.";
RL Genomics 47:207-216(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA MEDLINE=97349118; PubMed=9205122;
RA Yamada Y., Nezu J., Shimane M., Hirata Y.;
RT "Molecular cloning of a novel vascular endothelial growth factor,
RT VEGF-D.";
RL Genomics 42:483-488(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=98118549; PubMed=9435229;
RA Achen M.G., Jeltsch M., Kukk E., Maekinen T., Vitali A., Wilks A.F.,
RA Alitalo K., Stacker S.A.;
RT "Vascular endothelial growth factor D (VEGF-D) is a ligand for the
RT tyrosine kinases VEGF receptor 2 (Flk1) and VEGF receptor 3 (Flt4).";
RL Proc. Natl. Acad. Sci. U.S.A. 95:548-553(1998).
DR EMBL; Y12864; CAA73371.1;
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## RESULT 14

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DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE C-SIS PROTO-ONCOGENE (FRAGMENT).  
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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RC TISSUE=CHORIOCARCINOMA;  
RX MEDLINE=95388493; PubMed=7659502;  
RA Dirks R.P.H., Onnekink C., Jansen H.J., de Jong A., Bloemers H.P.J.;  
RT "A novel human c-sis mRNA species is transcribed from a promoter in c-  
RT sis intron 1 and contains the code for an alternative PDGF B-like  
RT protein.";  
RL Nucleic Acids Res. 23:2815-2822(1995).  
DR EMBL; X83705; CAA58679.1; -  
DR HSP; P01127; IPDG.

DR InterPro; IPR000072; -  
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Q9UF23 PRELIMINARY; PRT; 226 AA.  
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DT 01-MAY-2000 (Tremblrel. 13, Created)





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Date: Aug 18, 2001 3:47 AM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 Compugen Ltd.

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Database sequences: 1344157

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VERSION AX027935.1 GI:10188752  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1035)

AUTHORS Gordon,R.D., Dijkmans,J.J., Sprengel,J.J., Yon,J.R., Xu,J.,  
Gosiewska,A. and Dhanaraj,S.N.

TITLE Vascular endothelial growth factor-x

JOURNAL Patent: WO 0037641-A 3 29-JUN-2000;

GORDON ROBERT DOUGLAS (BE) ; DIJKMANS JOSTENA JOHANNA HUBER (BE) ;

JANSSEN PHARMACEUTICA NV (BE) ; SPRENGEL JORG JURGEN (BE) ; YON

JEFFREY ROLAND (BE) ; XU JEAN (US) ; GOSIEWSKA ANNA (US) ; DHANARAJ

SRIDEVI NAIDU (US)

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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Gordon,R.D., Dijkmans,J.J., Sprengel,J.J., Von,J.R., Xu,J.,  
Gosiewska,A. and Dhanaraj,S.N.  
TITLE Vascular endothelial growth factor-x  
JOURNAL Patent: WO 0037641-A 29-JUN-2000;  
GORDON ROBERT DOUGLAS (BE); DIJKMANS JOSIENA JOHANNA HUBER (BE);  
JANSSEN PHARMACEUTICA NV (BE); SPRENGEL JORG JURGEN (BE); YON  
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Gilbert,T., Hart,C.E., Sheppard,P.O. and Gilbertson,D.G.  
TITLE Growth factor homolog zvegfa  
JOURNAL Patent: WO 0066736-A 32-09-NOV-2000;  
ZymoGenetics, Inc. (US)  
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DEFINITION Homo sapiens hSCDGF mRNA for spinal cord-derived growth factor,
            complete cds.
ACCESSION  AB033831
VERSION    AB033831.1 GI:9392293
KEYWORDS   spinal cord-derived growth factor; scdGF gene.
SOURCE     Homo sapiens embryo brain cDNA to mRNA.
ORGANISM   Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (sites)
AUTHORS    Hamada,T., Ui-Tei,K. and Miyata,Y.
TITLE      A novel gene derived from developing spinal cords, SCDGF, is a
            unique member of the PDGF/VEGF family(1)
JOURNAL    FEBS Lett. 475 (2), 97-102 (2000)
MEDLINE    20317014
REFERENCE  2 (bases 1 to 1817)
AUTHORS    Hamada,T., Ui-Tei,K. and Miyata,Y.
TITLE      Direct Submission
JOURNAL    Submitted (25-OCT-1999) to the DDBJ/EMBL/GenBank databases.
            Tsuyoshi Hamada, Nippon Medical School, Department of Pharmacology;
            1-1-5, Sendagi, Bunkyo-ku, Tokyo 113-8602, Japan
            (E-mail:t-hamada@nms.ac.jp, Tel:81-3-3822-2131(ex.5277),
            Fax:81-3-5814-1684)

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DEFINITION Homo sapiens platelet-derived growth factor C mRNA, complete cds.
ACCESSION  AF244813
VERSION    AF244813.1 GI:8886883
KEYWORDS   human.
SOURCE     human.
ORGANISM   Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 2152)
AUTHORS    Li,X., Ponten,A., Aase,K., Karlsson,L., Abramsson,A., Utela,M.,
            Backstrom,G., Hellstrom,M., Bostrom,H., Li,H., Soriano,P.,
            Betsholtz,C., Heldin,C.-H., Alitalo,K., Ostman,A. and Eriksson,U.
            PDGF-C is a novel protease-activated ligand for the PDGF alpha
            receptor
            Nat. Cell Biol. (2000) In press
JOURNAL    2 (bases 1 to 2152)
REFERENCE  Eriksson,U., Aase,K., Li,X. and Ponten,A.
AUTHORS    Direct Submission
TITLE      Submitted (14-MAR-2000) Ludwig Institute for Cancer Research,
            Nobels vag 3 P.O.Box 240, Stockholm S-171 77, Sweden
JOURNAL    Location/Qualifiers
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VERSION AX047650.1 GI:11876693  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 2849)  
AUTHORS Baker,K.P., Chen,J., Ferrara,N., Fong,S., Goddard,A., Gurney,A.L.,  
Hillan,K.J., Kuo,S.S., Tumas,D. and Wood,W.I.  
TITLE Compositions and methods for the treatment of immune related  
diseases  
JOURNAL Patent: WO 0070050-A 9 23-NOV-2000;  
Genentech, Inc. (US)  
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DEFINITION Homo sapiens secretory growth factor-like protein fallotein mRNA, complete cds.  
ACCESSION AF091434  
VERSION AF091434.1 GI:6002592  
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REFERENCE 1 (bases 1 to 3007)  
AUTHORS Tsai, Y.-J., Lee, R.K.-K., Lin, S. and Chen, Y.  
TITLE Identification of a novel platelet-derived growth factor-like gene, fallotein, in the human reproductive tract  
JOURNAL Biochim. Biophys. Acta 1492 (1), 196-202 (2000)  
MEDLINE 20461776  
REFERENCE 2 (bases 1 to 3007)  
AUTHORS Tsai, Y.-J., Lee, R.K.-K. and Lin, S.P.  
TITLE Direct Submission  
JOURNAL Submitted (14-SEP-1998) Dept. Medical Research, Mackay Memorial Hospital, 45 Min Sheng Road, Tamshui, Taipei County 25115, Taiwan  
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DEFINITION Mus musculus fallotein mRNA, complete cds.  
ACCESSION AF117608  
VERSION AF117608.1 GI:6652867  
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ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE 1 (bases 1 to 2692)  
AUTHORS Tsai, Y.-J., Lee, R.K.-K., Chen, Y.-H., Lin, S.-P. and Cheng, W.T.-K.  
TITLE cDNA cloning of fallotein from mouse ovary  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 2692)  
AUTHORS Tsai, Y.-J., Lee, R.K.-K., Chen, Y.-H., Lin, S.-P. and Cheng, W.T.-K.  
TITLE Direct Submission  
JOURNAL Submitted (03-JAN-1999) Medical Research, Mackay Memorial Hospital, 45 Min Sheng Road, Tamshui, Taipei 25115, Taiwan  
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ACCESSION AX044520
VERSION AX044520.1 GI:11343375
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SOURCE house mouse.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
AUTHORS Gilbert,T., Hart,C.E., Sheppard,P.O. and Gilbertson,D.G.
TITLE Growth factor homolog zveg14
JOURNAL Patent: WO 0066736-A 34 03-NOV-2000;
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DEFINITION Mus musculus platelet-derived growth factor C (pdgfc) mRNA,
complete cds.
ACCESSION AF286725
VERSION AF286725.1 GI:9652343
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
AUTHORS Ding,H., Wu,X., Kim,I., Tam,P.P., Koh,G.Y. and Nagy,A.
TITLE The mouse pdgfc gene: dynamic expression in embryonic tissues
during organogenesis
JOURNAL Mech. Dev. 96 (2), 209-213 (2000)
MEDLINE 20417814
REFERENCE 2 (bases 1 to 1038)
AUTHORS Ding,H., Wu,X., Tam,P.P.L. and Nagy,A.
TITLE Direct Submission
JOURNAL Submitted (12-JUL-2000) Samuel Lunenfeld Research Institute, Mount
Sinai Hospital, 600 University Avenue, Toronto, Ontario M5G 1X5,
Canada
FEATURES Location/Qualifiers
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LOCUS AB033830 1116 bp mRNA 10-FEB-2001  
DEFINITION Rattus norvegicus rScdglf mRNA for spinal cord-derived growth factor, complete cds.  
ACCESSION AB033830  
VERSION AB033830.1 GI:11994799  
KEYWORDS spinal cord-derived growth factor; SCDFG.  
SOURCE Rattus norvegicus (strain:Wistar) Adult Kidney cDNA to mRNA.  
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REFERENCE 1 (sites)  
AUTHORS Hamada,T., Ui-Tei,K., Imaki,J. and Miyata,Y.  
TITLE Molecular Cloning of SCDFG-B, a Novel Growth Factor Homologous to SCDFG/PDGF-C/falotekin  
JOURNAL Biochem. Biophys. Res. Commun. 280 (3), 733-737 (2001)  
PUBMED 11162582  
REFERENCE 2 (bases 1 to 1116)  
AUTHORS Hamada,T., Ui-Tei,K. and Miyata,Y.  
TITLE Direct Submission  
JOURNAL Submitted (25-OCT-1999) Tsuyoshi Hamada, Nippon Medical School, Department of Pharmacology, 1-1-5, Sendagi, Bunkyo-ku, Tokyo 113-8602, Japan (E-mail:t-hamada@nms.ac.jp, Tel:81-3-3822-2131(ex.5277), Fax:81-3-5814-1684)

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DEFINITION Gallus gallus SCDGF mRNA for spinal cord-derived growth factor,
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ACCESSION AB033829
VERSION AB033829.1 GI:9392291
KEYWORDS spinal cord-derived growth factor; scdgf gene.
SOURCE Gallus gallus (strain:white leghorn) embryo spinal cord cdna to
mRNA.
ORGANISM Gallus gallus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (sites)
Hamada,T., Ui-Tei,K. and Miyata,Y.
A novel gene derived from developing spinal cords, SCDGF, is a
unique member of the PDGF/VEGF family(1)
FEBS Lett. 475 (2), 97-102 (2000)
20317014
2 (bases 1 to 1675)
Hamada,T., Ui-Tei,K. and Miyata,Y.
Direct Submission
Submitted (25-OCT-1999) to the DBJ/EMBL/GenBank databases.
Tsuyoshi Hamada, Nippon Medical School, Department of Pharmacology;
1-1-5, Sendagi, Bunkyo-ku, Tokyo 113-8602, Japan
(E-mail:t-hamada@nms.ac.jp, Tel:81-3-3822-2131(ex.5277),
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gene

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DEFINITION Sequence 36 from Patent WO0037641.
ACCESSION AX027968
VERSION AX027968.1 GI:10188782
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequence.
REFERENCE 1 (bases 1 to 279)
AUTHORS Gordon,R.D., Dijkmans,J.J., Sprengel,J.J., Yon,J.R., Xu,J.,
Gosiewska,A. and Dhanaraj,S.N.
Vascular endothelial growth factor-x
Patent: WO 0037641-A 36 29-JUN-2000;
GORDON ROBERT DOUGLAS (BE) ; DIJKMANS JOSTENA JOHANNA HUBER (BE) ;
JANSEN PHARMACEUTICA NV (BE) ; SPRENGEL JORG JURGEN (BE) ; YON
JEFFREY ROLAND (BE) ; XU JEAN (US) ; GOSIEWSKA ANNA (US) ; DHANARAJ
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ACCESSION AX027989
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ORGANISM
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REFERENCE
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AUTHORS
Gordon,R.D., Dijkmans,J.J., Sprengel,J.J., Yon,J.R., Xu,J.,
Gosiewska,A. and Dhanaraj,S.N.
TITLE
Vascular endothelial growth factor-x
JOURNAL
Patent: WO 0037641-A 57 29-JUN-2000;
GORDON ROBERT DOUGLAS (BE) ; DIJKMANS JOSIENA JOHANNA HUBER (BE) ;
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REFERENCE
1 (bases 1 to 279)
AUTHORS
Gordon,R.D., Dijkmans,J.J., Sprengel,J.J., Yon,J.R., Xu,J.,
Gosiewska,A. and Dhanaraj,S.N.
TITLE
Vascular endothelial growth factor-x
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GORDON ROBERT DOUGLAS (BE) ; DIJKMANS JOSIENA JOHANNA HUBER (BE) ;
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; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: Steven A. STACKER
; APPLICANT: Kari ALITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street, NW, Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: United States of America
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,795
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/42983
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 6:
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US-09-457-066-2_COPY_210_345 x US-08-915-795-6
Align seg 1/1 to: US-08-915-795-6 from: 1 to: 1325

29  LeuAsnLeuLeuThrGluGluValArgLeuTyrSerCysThrProArgAs 45
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
391 CTAAAGTTATAGATGAAGATGCGAGAGACCCCAATGACGCCCTAGAGA 440

45  nPheSerValSerIleArgGluGluLeu...LysArgThrAspThrIleP 61
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
441 GACATCGCTAGAAGTCGCCAGTGAGCTGGGAAGACACAACCAACATCT 490

61  heTTPProGlyCysLeuLeuValLysArgCysGlyGlyAsnCysAlaCys 77
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
491 TCAAGCCCCCTGTGTAAATGCTCTCGGTGTGAGGC.....TGC 531

78  CysLeuHisAsnCysAsnGluCysGlnCysVal.....ProSerLy 91
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
532 TGC.....AACGAGAGGGTGTGTATGATGAACAACAGCACCTCCTA 575

91  sValThrLysLysTyRHISgluValLeuGlnLeuArgProLysThrGlyV 108
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
576 CATCTCCAAACAGCTCTTTGAGATATCAGTG.....CCTCTGACATCAG 619

108 aLArgGlyLeuHisLysSerLeuThrAspValAlaLeuGluHisGlu 124
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
620 TG.....CCCGAGTTAGTCTGTAAATTTGCCAACCACATACG 657

125 GluCysAspCysValCysArgGly 132
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658 GGTGTGAAGTGTGCCACGGGC 681

seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-08-915-795-4

seq_documentation_block:
; Sequence 4, Application US/08915795
; Patent No. 6235713
; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: Steven A. STACKER
; APPLICANT: Kari ALITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street, NW, Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: United States of America
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,795
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/42983
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2029 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Human Lung
;
US-08-915-795-4

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alignment_scores:
  Quality: 116.00      Length: 152
  Ratio: 1.506        Gaps: 8
  Percent Similarity: 50.658      Percent Identity: 28.289

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US-09-457-066-2_COPY_210_345 x US-08-915-795-4
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Align seg 1/1 to: US-08-915-795-4 from: 1 to: 2029
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558 TTGGAGGAACACTTGAATTAACCTCACTCTGAGGACTGGAAGCTGTGGAG 607
14 .....LeuGlyLysAlaPheValP 20
|||||:||||| ||| ||| |||:|||||
608 ATCAGAGCTGAGGCTCAAAAGCTTTTACCAGTATGAGACTTCGCTCAGCAT 657
20 heGlyArgLysSerArg.....ValValAspLeu 29
|||||:||||| ||| ||| |||:|||||
658 CCCATCGGTCCACTAGGTTTCGGCAACTTCTATGACATTGAAACACATP 707
30 AsnLeuLeuThrGluValArgLeuTyrSerCysThrProArgAsnPh 46
|||||:||||| ||| ||| |||:|||||
708 AAAGTTATAGATGAAGATGCAAGAAGACTCAGTCAGCGCCCTAGAGAAAC 757
46 eSerValSerIleArgGluGluLeu...LysArgThrAspThrIlePheT 62
|||||:||||| ||| ||| |||:|||||
758 GTGCGTGGAGGTGGCCAGTCTGATGACACACCAGCCTCGTACATTCCAA 807
62 rpProGlyCysLeuLeuValLysArgCysGlyGlyAsnCysAlaCysCys 78
|||||:||||| ||| ||| |||:|||||
808 AGCCCCCTTGTGTAACCTGTTCCGATGTGGTGGC.....TGTTCG 848
79 LeuHisAsnCysAsnGluCys...GlnCysValProSerLysValThrLy 94
|||||:||||| ||| ||| |||:|||||
849 AATGAGAGAGCCCTATCTGTATGACACACCAGCCTCGTACATTCCAA 898
94 sLysTyrHisGluValLeuGlnLeuArgProLysThrGlyValArgGlyL 111
|||||:||||| ||| ||| |||:|||||
899 ACAGCTCTTTGAGATATCAGTG.....CCTTTGACATCAGTA..... 935
111 euHisLysSerLeuThrAspValAlaLeuGluHisGluCysAsp 127
|||||:||||| ||| ||| |||:|||||
936 .....CTGAATTAGTCTGTTAAAGTTGCCAATCATACAGGTTCTTAAG 980
128 CysVal 129
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; Sequence 1, Application US/08915795
; Patent No. 6235713
;
GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: Steven A. STACKER
; APPLICANT: Kari ALITALO
;
TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:

```

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; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street, NW, Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: United States of America
; ZIP: 20005
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,795
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/42983
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2846 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Human Breast
;
US-08-915-795-1

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alignment_scores:
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  Quality: 116.00      Length: 152
  Ratio: 1.506        Gaps: 8
  Percent Similarity: 50.658      Percent Identity: 28.289

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alignment_block:
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US-09-457-066-2_COPY_210_345 x US-08-915-795-1
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Align seg 1/1 to: US-08-915-795-1 from: 1 to: 2846
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14 .....LeuGlyLysAlaPheValP 20
|||||:||||| ||| ||| |||:|||||
1881 ATCAGAGCTGAGGCTCAAAAGCTTTTACCAGTATGAGACTTCGCTCAGCAT 1930
20 heGlyArgLysSerArg.....ValValAspLeu 29
|||||:||||| ||| ||| |||:|||||
1931 CCCATCGGTCCACTAGGTTTCGGCAACTTCTATGACATTGAAACACATA 1980
30 AsnLeuLeuThrGluValArgLeuTyrSerCysThrProArgAsnPh 46
|||||:||||| ||| ||| |||:|||||
1981 AAAGTTATAGATGAAGATGCAAGAAGACTCAGTCAGCGCCCTAGAGAAAC 2030
46 eSerValSerIleArgGluGluLeu...LysArgThrAspThrIlePheT 62
|||||:||||| ||| ||| |||:|||||
2031 GTGCGTGGAGGTGGCCAGTCTGATGACACACCAGCCTCGTACATTCTTCA 2080
62 rpProGlyCysLeuLeuValLysArgCysGlyGlyAsnCysAlaCysCys 78
|||||:||||| ||| ||| |||:|||||
2081 AGCCCCCTTGTGTAACCTGTTCCGATGTGGTGGC.....TGTTCG 2121
79 LeuHisAsnCysAsnGluCys...GlnCysValProSerLysValThrLy 94
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2122 AATGAGAGAGCCCTTATCTGTATGAAACACCAGCCTCGTACATTCCAA 2171

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324 ATCGTGAAACCAGCTATGATCGCTGAATGTAAAGACTAGAACTAAGTTTC 275
47 rValSerIleArgGluGluLeuLysArgThrAspThrIlePhe.....T 62
   | ||| : : : : : : : : ||||| : : : : : |||
274 GAAATCTCCAGAGATTTCGATCGACAGAACTAACGCTAACTTCTGGTTT 225
62 rpProGlyCysLeuLeuValLysArgCysGlyGlyAsnCysAlaCysCys 78
   ||| |||| : : : : : ||||| : : : : : |||
224 GGCACCATGTGTTGAAGTTCAAGATGTTCTGCT.....TGTGT 184
79 LeuHisAsnCysAsnGluCysGlnCysValProSerLysValThrLysLys 95
   ||| |||| : : : : : ||||| : : : : : |||
183 .....AACAAACGAAACGTTCAATGTAGACCAACTCAAGTT..... 148
95 sTyrHisGluValLeuGlnLeuArgPro.....LysThrGlyV 108
   ||||| ||||| ||||| : : : : :
147 .....CAATTGAGACCAGTTCAGTTAGAAAGATCGAAA 114
108 al.....ArgGlyLeuHisLysSerLeuThrAspValAlaLeuGlu 121
   : : : : : : : : ||| : : : : : |||
113 TCGTTAGAAAGAACCAACTCTTCAAGAAGGCTACT...GTTACTTTGGAA 67
122 HisHisGluGluCysAspCys 128
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66 GACCACCTGGCTGTGTAAGTGT 46

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seq\_name: /cqn2\_6/ptodata/1/ina/6A\_COMB.seq:US-09-340-250-4

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seq_documentation_block:
; Sequence 4, Application US/09340250
; Patent No. 6083723
; GENERAL INFORMATION:
; APPLICANT: Tekamp-Olson, Patricia
; TITLE OF INVENTION: METHOD FOR EXPRESSION OF HETEROLOGOUS
; TITLE OF INVENTION: PROTEINS IN YEAST
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell Sellzer IP Group of Alston & Bird, LLP
; STREET: 3605 Glenwood Ave. Suite 310
; CITY: Raleigh
; STATE: NC
; COUNTRY: US
; ZIP: 27622
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/340,250
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/989,251
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: 5784-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919 420 2202
; TELEFAX: 919 881 3175
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Complementing strand to the
; DESCRIPTION: preceding SEQ ID NO.; listed to show the
; DESCRIPTION: produced upon assembly."
; ORIGINAL SOURCE:

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alignment\_block:  
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seq_name: /cgn2_6/ptodata/1/ina/backfiles1.seq:5175255-3
seq_documentation_block:
; Patent No. 5175255
; APPLICANT: Thomson, Arlen R. Nicholson, Margery
; TITLE OF INVENTION: METHODS FOR PURIFICATION OF PLATELET-
; DERIVED GROWTH FACTOR
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/06/25,344
; FILING DATE: 23-MAR-1987
; SEQ ID NO:3:
; LENGTH: 691
5175255-3

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三三三



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222 GAGCTGGAGAGCTTGGCTCGT..... 242
18 eValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThr.... 33
  ::::::::::::::|||
243 .....GGAAGAGGAGC.....CTGGTTCCTGACCATG 273
34 ..GluGluValArgLeuTySerCysThrProArgAsn.....PheSer 47
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274 CTGAGCGCGCATGATCGCGAGTCAAGAGCGCGCACCGAGGTGTTGAG 323
48 ValSerIleArgGluGluLeuLysArgThrAspThrIlePhe.....Tr 62
  ::||| ::||| ::||| ::||| ::|||
324 ATCTCC...CGGCGCTCATAGACCGCACCAACGCAACTTCTGCTGTG 370
62 pProGlyCysLeuLeuValLysArgCysGlyGlyAsnCysAlaCysCysL 79
  ||| ||| ::||| ::||| ::|||
371 GCCGCCCTGTGTGAGGTGACGCGTCTCGGC.....TGCTGC. 410
79 euHisAsnCysAsnGluCysGlnCysValProSerLysValThrLysLys 95
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411 .....AACACCGGAAGAGTGCAGTGCCTGCCGCCACCCAGGTG..... 446
96 TyrHisGluValLeuGlnLeuArgPro.....LysThrGlyVa 108
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447 .....CAGCTGCAGCTGTGCAGGTGAGAAAGATCGAGAT 481
108 1.....ArgGlyLeuHisLysSerLeuThrAspValAlaLeuGluH 122
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482 TGTGCGGAAGAGCAATCTTTAGAGAGGCCACG...GTGAGCTGGAAG 528
122 isHisGluGluCysAspCys 128
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seq\_name: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:US-08-387-845-3

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seq_documentation_block:
; Sequence 3, Application US/08387845
; Patent No. 5665567
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Preparation of heterodimeric PDGF-AB using a
; TITLE OF INVENTION: bicistronic vector system in mammalian cells
; NUMBER OF SEQUENCES: 16
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPA)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,845
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 868 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: pMW-2 (Weich et al., 1986)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 40..762
; OTHER INFORMATION: /product= "PDGF-B
; OTHER INFORMATION: precursor sequence"
; OTHER INFORMATION: /note= "human PDGF-B gene from pGEM2-PDGF-B,

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; OTHER INFORMATION: flanked by 5'-EcoRI und 3'-HindIII
; OTHER INFORMATION: restriction cleavage sites"
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 283..609
; OTHER INFORMATION: /product= "mature PDGF-B chain"
; PUBLICATION INFORMATION:
; AUTHORS: Weich, H. A.
; AUTHORS: Seibald, W.
; AUTHORS: Schairer, H. U.
; AUTHORS: Hoppe, U.
; JOURNAL: FEBS Lett.
; VOLUME: 198
; PAGES: 344-348
; DATE: 1986
; US-08-387-845-3

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alignment_scores:
  Quality: 110.00      Length: 140
  Ratio: 1.528        Gaps: 12
  Percent Similarity: 51.429    Percent Identity: 32.857
alignment_block:
US-09-457-066-2_copy_210_345 x US-08-387-845-3
Align seg 1/1 to: US-08-387-845-3 from: 1 to: 868

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253 GAGCTGGAGAGCTTGGCTCGT..... 273
18 eValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThr.... 33
  ::||| ::||| ::||| ::|||
274 .....GGAAGAGGAGC.....CTGGTTCCTGACCATG 304
34 ..GluGluValArgLeuTySerCysThrProArgAsn.....PheSer 47
  ||| :: :: :: :: |||
305 CTGAGCGCGCATGATCGCGAGTCAAGAGCGCGCACCGAGGTGTTGAG 354
48 ValSerIleArgGluGluLeuLysArgThrAspThrIlePhe.....Tr 62
  ::||| ::||| ::||| ::|||
355 ATCTCC...CGGCGCTCATAGACCGCACCAACGCAACTTCTGCTGTG 401
62 pProGlyCysLeuLeuValLysArgCysGlyGlyAsnCysAlaCysCysL 79
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402 GCCGCCCTGTGTGAGGTGACGCGTCTCGGC.....TGCTGC. 441
79 euHisAsnCysAsnGluCysGlnCysValProSerLysValThrLysLys 95
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442 .....AACACCGGAAGAGTGCAGTGCCTGCCGCCACCCAGGTG..... 477
96 TyrHisGluValLeuGlnLeuArgPro.....LysThrGlyVa 108
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478 .....CAGCTGCAGCTGTGCAGGTGAGAAAGATCGAGAT 512
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seq_documentation_block:
; Sequence 3, Application US/08778275
; Patent No. 5935819
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Preparation of heterodimeric PDGF-AB using a
; TITLE OF INVENTION: bicistronic vector system in mammalian cells

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DATE: 1986  
US-08-867-352-3

alignment\_scores:  
Quality: 110.00 Length: 140  
Ratio: 1.528 Gaps: 12  
Percent Similarity: 51.429 Percent Identity: 32.857

alignment\_block:  
US-09-457-066-2\_COPY\_210\_345 x US-08-867-352-3 ..  
Align seg 1/1 to: US-08-867-352-3 from: 1 to: 868

2 AspLeuGluAspLeuTyArgProThrTrpGlnLeuLeuGlyLysAlaPh 18  
253 GAGCTGGAGAGCTTGGCTCGT.....CTGGTTCCCTGACCATTTG 273  
18 eValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThr.... 33  
274 .....GGAAGAAGGAGC.....CTGGTTCCCTGACCATTTG 304  
34 ..GluGluValArgLeuTySerCysThrProArgAsn.....PheSer 47  
305 CTGAGCGCGCATGATCCCGAGTGCAGACCGCGACCGAGGTGTTCGAG 354  
48 ValSerIleArgGluGluLeuLysArgThrAspThrIlePhe.....Tr 62  
355 ATCTCC...CGCGCGCTCATAGACCGCACCAAGCGCAACTTCTGCTGTG 401  
62 pProGlyCysLeuLeuValLysArgCysGlyGlyAsnCysAlaCysCysL 79  
402 GCCGCCCTGTCTGAGGTGTCAGCGTGTCTCCGCC.....TGCTGC. 441  
79 euHisAsnCysAsnGlyCysGlnCysValProSerLysValThrLysLys 95  
442 .....ACAACCGCACTGTCAGTCCGCCCCACCCAGGTG..... 477  
96 TyrHisGluValLeuGlnLeuArgPro.....LysThrGlyVa 108  
478 .....CAGCTGGACCTTCCAGGTGAGAAAGATCGAGAT 512  
108 l.....ArgGlyLeuHisLysSerLeuThrAspValAlaLeuGluH 122  
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122 isHisGluGluCysAspCys 128  
560 ACCACCTGGCATGCAAGTGT 579

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seq\_documentation\_block:  
Sequence 28, Application US/08989251  
Patent No. 6017731  
GENERAL INFORMATION:  
APPLICANT: Tekamp-Olson, Patricia  
TITLE OF INVENTION: METHOD FOR EXPRESSION OF HETEROLOGOUS  
TITLE OF INVENTION: PROTEINS IN YEAST  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bell Seltzer IP Group of Alston & Bird, LLP  
STREET: 3605 Glenwood Ave. Suite 310  
CITY: Raleigh  
STATE: NC  
COUNTRY: US  
ZIP: 27622  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/989,251  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Spruill, W. Murray  
REGISTRATION NUMBER: 32,943  
REFERENCE/DOCKET NUMBER: 5784-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919 420 2202  
TELEFAX: 919 881 3175  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1320 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "Synthetic chimera"  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens/Saccharomyces cerevisiae  
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LOCATION: 454..519  
OTHER INFORMATION: /product= "PDGF-B prepeptide"  
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NAME/KEY: transit\_peptide  
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OTHER INFORMATION: /function= "mediates protein  
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OTHER INFORMATION: /standard\_name= "PDGF-B presequence"  
US-08-989-251-28

alignment\_scores:  
Quality: 110.00 Length: 140  
Ratio: 1.528 Gaps: 12  
Percent Similarity: 51.429 Percent Identity: 32.857

alignment\_block:  
US-09-457-066-2\_COPY\_210\_345 x US-08-989-251-28 ..  
Align seg 1/1 to: US-08-989-251-28 from: 1 to: 1320  
2 AspLeuGluAspLeuTyArgProThrTrpGlnLeuLeuGlyLysAlaPh 18  
667 GAGCTGGAGAGCTTGGCTCGT.....CTGGTTCCCTGACCATTTG 718  
18 eValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThr.... 33  
688 .....GGAAGAAGGAGC.....CTGGTTCCCTGACCATTTG 718  
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; Patent No. 6083723
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; APPLICANT: Tekamp-Olson, Patricia
; TITLE OF INVENTION: METHOD FOR EXPRESSION OF HETEROLOGOUS
; TITLE OF INVENTION: PROTEINS IN YEAST
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell Seltzer IP Group of Alston & Bird, LLP
; STREET: 3605 Glenwood Ave. Suite 310
; CITY: Raleigh
; STATE: NC
; COUNTRY: US
; ZIP: 27622
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/340,250
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/989,251
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: 5784-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919 420 2202
; TELEFAX: 919 881 3175
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1320 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Synthetic chimera"
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens/Saccharomyces cerevisiae
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; NAME/KEY: CDS
; LOCATION: 454..1179
; FEATURE:
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688 .....GGAAGAGAGGAGC.....CTGGGTTCCCTGACCATG 718

34 ..GluGluValArgLeuTyrSerCysThrProArgAsn.....PheSer 47
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48 ValSerIleArgGluGluLeuLysArgThrAspThrIlePhe.....Tr 62
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79 euHisAsnCysAsnGluCysGlnCysValProSerLysValThrLysLys 95
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96 TyrHisGluValLeuGlnLeuArgPro.....LysThrGlyVa 108
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892 .....CAGCTGCACCTGTCCAGGTGAGAAAGATCGAGAT 926

108 1.....ArgGlyLeuHisLysSerLeuThrAspValAlaLeuGluH 122
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927 TGTGCGGAAGAACCCATCTTTAAGRAGGCCAGC...GTGACGCTGGAAG 973

122 isHisGluLucyAspCys 128
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Date: Aug 18, 2001 4:13 AM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 CompuGen Ltd.

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Search information block:

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seq\_documentation\_block:

ID AAA51540 standard; cDNA; 1095 BP.

AC AAA51540;

DT 26-SEP-2000 (first entry)

DE MBP-ZVEGF3 fusion protein coding sequence.

KW Vascular endothelial growth factor; homologue; zvegf3; CUB domain;  
KW Cysteine knot; platelet-derived growth factor; PDGF; neuropilin;  
KW Chromosome 4q28.3; cytostatic; anti-psoriatic; anti-inflammatory;  
KW anti-diabetic; ophthalmological; anti-rheumatic; anti-arthritis;  
KW vulnary; maltose binding protein; MBP; ss.

OS Chimeric - Homo sapiens.

OS Chimeric - Synthetic.

PN WO200034474-A2.

PD 15-JUN-2000.

PF 07-DEC-1999; 99WO-US28968.

PR 07-DEC-1999; 98US-0207120.

PR 06-JUL-1999; 99US-0142576.

PR 21-OCT-1999; 99US-0161653.

PR 12-NOV-1999; 99US-0165255.

(ZYMO ) ZYMOGENETICS INC.

Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KE;

Gilbertson DG, West JW;

WPI; 2000-423420/36.

Novel zvegf3 polypeptides and nucleotides encoding them useful for  
stimulating growth of smooth muscle cells and fibroblasts comprising an  
epitope bearing portion of a specific amino acid sequence

Example 28; Page 172-173; 173pp; English.

This DNA encodes human ZVEGF3 (a novel vascular endothelial growth  
factor homologue) fused N-terminally to maltose binding protein (MBP).  
Polypeptides comprising an epitope-bearing portion human or murine  
ZVEGF3 are claimed. The growth factors comprise a growth factor domain  
and a CUB domain (genetic sequence motifs are shown in AA96859 and  
AA96860). The growth factor domain is characterized by an arrangement of  
cysteine residues and beta-strands that is characteristic of the  
"cysteine knot" structure of the platelet-derived growth factor (PDGF)  
family. The CUB domain shows homology to CUB domains in neuropilins,  
human bone morphogenetic protein-1, porcine seminal plasma protein,  
bovine acidic seminal fluid protein and Xenopus laevis tolloid-like  
protein. Structural analysis and homology predict that ZVEGF3  
polypeptides complex with a second polypeptide to form multimeric  
proteins. The human zvegf3 gene has been mapped to chromosome 4q28.3.

ZVEGF3 is useful for stimulating the growth of fibroblasts or smooth  
muscle cells, for activating cell surface PDGF-alpha receptor and for  
inhibiting PDGF-alpha receptor mediated cellular processes. ZVEGF3 is  
useful for regulating (post-development) organ growth, regeneration and  
maintenance, as well as tissue maintenance and repair processes. ZVEGF3  
antagonists are useful for treating cancer, rheumatoid arthritis,  
diabetic retinopathy, ischemic limb disease, peripheral vascular  
disease, myocardial ischemia, vascular intimal hyperplasia, atherosclerosis, wound  
healing, chronic liver disease and haemangioma formation. ZVEGF3 can also

CC be used to modulate neurite growth and development of the nervous system,  
CC and for treating neurodegenerative diseases.

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Ratio: 5.544 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

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|||||  
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34 luGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerIle 50  
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767 AGGAGGTAAAGATTATACAGCTGCACACCTCGTAACCTCTCAGTGTCCATA 816  
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817 AGGGAAGAACTAAAGAGAACCGATACCATTTTCTGCCAGGTTGTCTCT 866  
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917 AATGTCAATGTCTCCCAAGCAAGTTACTAAAAATACCAAGGTCCT 966  
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seq\_documentation\_block:

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XX AA

XX AA

DT 19-JAN-2001 (first entry)

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XX DE

XX DE

KW VEGF-X; vascular endothelial growth factor; human; vulnary; cytostatic;

KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;

KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;

KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;

KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;

KW venous sore; diabetic ulcer; burns; skin graft growth; ds.

XX OS

XX Homo sapiens.

XX Key

FH Location/Qualifiers

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PN WO200037641-A2.

XX 29-JUN-2000.

XX 21-DEC-1999; 99WO-US30503.

XX 22-DEC-1998; 98GB-0028377.

XX 18-MAR-1999; 99US-0124967.

XX 08-NOV-1999; 99US-0164131.

XX (JANC ) JANSSEN PHARM NV.

XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;

XX Dhanaraj SN, Xu J;

XX WPI; 2000-442669/38.

XX P-PSDB; AAB10641.

XX New vascular endothelial growth factor protein, useful for treating or

XX preventing diseases associated with inappropriate angiogenesis activity

XX such as cancer, rheumatoid arthritis, psoriasis and wounds -

XX Disclosure; Fig 21; 127pp; English.

XX This invention describes a novel vascular endothelial growth factor-X

XX (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has

XX vulnary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and

XX antidiabetic activity and acts as an angiogenesis and vascularization

XX regulator. An antisense molecule of the invention is useful for treating

XX or preventing cancer, rheumatoid arthritis, psoriasis and diabetic

XX retinopathy by inhibiting angiogenic activity or inappropriate

XX vascularization including formation and proliferation of new blood

XX vessels, growth and development of tissues, tissue regeneration and organ

XX and tissue repair in a subject. The products of the invention are useful

XX for preparing medicaments for treating wounds such as dermal ulcers,

XX pressure sores, venous sores, diabetic ulcers and burns and to promote

XX skin graft growth, tissue repair, proliferation of new blood vessels,

XX tissue regeneration and organ repair by promoting angiogenic activity or

XX vascularization. This sequence encodes a human VEGF-X protein which can

XX be expressed in E. coli systems and which is described in the method of

XX the invention.

XX SQ Sequence 1096 BP; 337 A; 225 C; 253 G; 281 T; 0 other;

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Quality: 754.00 Length: 136

Ratio: 5.544 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-457-066-2\_COPY\_210\_345 x AAA71985

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17 aPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThrG 34

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692 TTTTGTGTTTGGAGAAAATCCAGAGTGTGTGATCTGAACCTTCTAACAG 741

34 luGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerIle 50

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742 AGGAGGTAAAGATTATACAGCTGCACACCTCGTAACCTCTCAGTGTCCATA 791

51 ArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeuLe 67

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seq\_documentation\_block:  
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DT  
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DE

Human VEGF-X DNA for expression in mammalian systems.  
XX  
KW VEGF-X; vascular endothelial growth factor; human; vulnary; cytostatic;  
KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;  
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;  
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;  
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;  
KW venous sore; diabetic ulcer; burns; skin graft growth; ds.  
XX  
OS Homo sapiens.

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PN WO200037641-A2.  
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PD 29-JUN-2000.  
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PF 21-DEC-1999; 99WO-US30503.  
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PR 22-DEC-1998; 98GB-0028377.  
PR 18-MAR-1999; 99US-0124967.  
PR 08-NOV-1999; 99US-0164131.  
XX  
PA (JANC ) JANSSEN PHARM NV.  
XX  
XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JH, Gosiewska A;  
PI Dhanaraj SN, Xu J;  
XX  
XX WPI: 2000-442669/38.  
XX P-PSDB; AAB10639.  
XX

New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -  
Disclosure; Fig 19; 127pp; English.  
XX  
PT This invention describes a novel vascular endothelial growth factor-x  
CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has

CC vulnary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and  
CC antidiabetic activity and acts as an angiogenesis and vascularization  
CC regulator. An antisense molecule of the invention is useful for treating  
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic  
CC retinopathy by inhibiting angiogenic activity or inappropriate  
CC vascularization including formation and proliferation of new blood  
CC vessels, growth and development of tissues, tissue regeneration and organ  
CC and tissue repair in a subject. The products of the invention are useful  
CC for preparing medicaments for treating wounds such as dermal ulcers,  
CC pressure sores, venous sores, diabetic ulcers and burns and to promote  
CC skin graft growth, tissue repair, proliferation of new blood vessels,  
CC tissue regeneration and organ repair by promoting angiogenic activity or  
CC vascularization. This sequence encodes a human VEGF-X protein which can  
CC be expressed in mammalian systems and which is described in the method of  
XX the invention.  
SQ Sequence 1134 BP; 324 A; 247 C; 269 G; 294 T; 0 other;

alignment\_scores:  
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Ratio: 5.54 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

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17 aPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThrG 34  
687 TTTTGTGTTTGGAGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAG 736  
34 luGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerile 50  
737 AGGAGGTAGATTATACAGCTGCACACTCGTAACCTCTCAGTGTCCATA 786  
51 ArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeuLe 67  
787 AGGGAAGAACTAAAGAGAACCCGATACCATTTTCTGGCCAGGTTGCTCCT 836  
67 uValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsnG 84  
837 GGTAAACCGCTGTGGTGGGAACCTGTGCCTGTGTCTCCACAATTCGAATG 886  
84 luCysGlnCysValProSerLysValThrLysLysLysHisGluValLeu 100  
887 AATGTCATGTGTCCCAAGCAAGTTACTAAATAATACCAGAGTCCCT 936  
101 GlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThrAs 117  
937 CAGTTGAGACCAAGACCGGTGTACGGGATTCACAAATCACTACCGA 986  
117 pValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySerT 134  
987 CGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGTCAGAGGAGCA 1036  
134 hrGlyGly 136  
1037 CAGGAGGA 1044

seq\_name: /SIDS8/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA71984  
seq\_documentation\_block:  
ID AAA71984 standard; DNA; 1134 BP.  
XX  
AC  
XX  
DT 19-JAN-2001 (first entry)



XX DE Human VEGF-X DNA for expression in Baculovirus/insect cell systems.

XX KW VEGF-X; vascular endothelial growth factor; human; vulnerary; cytotstatic;

XX KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;

XX KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;

XX KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;

XX KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;

XX KW venous sore; diabetic ulcer; burns; skin graft growth; ds.

OS Homo sapiens.

EH Key Location/Qualifiers

FT CDS 63..1127

FT /\*tag= a

FT /product= "VEGF-X"

XX PN WO200037641-A2.

XX PD 29-JUN-2000.

XX PF 21-DEC-1999; 99WO-US30503.

XX PR 22-DEC-1998; 98GB-0028377.

XX PR 18-MAR-1999; 99US-0124967.

XX PR 08-NOV-1999; 99US-0164131.

XX PA (JANC ) JANSSEN PHARM NV.

XX PI Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;

XX PI Dhanaraj SN, Xu J;

XX DR WPI; 2000-442669/38.

XX DR P-PSDB; AAB10640.

XX PT New vascular endothelial growth factor protein, useful for treating or

XX PT preventing diseases associated with inappropriate angiogenesis activity

XX PT such as cancer, rheumatoid arthritis, psoriasis and wounds -

XX PS Disclosure; Fig 20; 127pp; English.

XX CC This invention describes a novel vascular endothelial growth factor-X

XX CC (VEGF-X) protein (Ia) and its encoding polynucleotide (Iia) which has

XX CC vulnerary, cytotstatic, antirheumatic, antiarthritic, antipsoriatic and

XX CC antidiabetic activity and acts as an angiogenesis and vascularization

XX CC regulator. An antisense molecule of the invention is useful for treating

XX CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic

XX CC retinopathy by inhibiting angiogenic activity or inappropriate

XX CC vascularization including formation and proliferation of new blood

XX CC vessels, growth and development of tissues, tissue regeneration and organ

XX CC and tissue repair in a subject. The products of the invention are useful

XX CC for preparing medicaments for treating wounds such as dermal ulcers,

XX CC pressure sores, venous sores, diabetic ulcers and burns and to promote

XX CC skin graft growth, tissue repair, proliferation of new blood vessels,

XX CC tissue regeneration and organ repair by promoting angiogenic activity or

XX CC vascularization. This sequence encodes a human VEGF-X protein which can

XX CC be expressed in Baculovirus/insect cell systems and which is described in

XX CC the method of the invention.

SQ Sequence 1134 BP; 339 A; 225 C; 254 G; 316 T; 0 other;

alignment\_scores:

Quality:	754.00	Length:	136
Ratio:	5.544	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000

alignment\_block:

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..f. +

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717 TTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAGGC 766

17 apheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThrG 34

|||||

767 TTTTGTTTTGGAGAAATCCAGAGTGGTGATCTGAACCTTCTTAACAG 816

34 luGluValArgLeuTyrSerCysThrProArgAsnPheserValserIle 50

|||||

817 AGGAGGTAAAGATTATACAGCTCCACACCTCGTAACCTTCTCAGTGTCCATA 866

51 ArgGluLeuLeuLysArgThrAspThrIlePheTrpProGlyCysLeuLe 67

|||||

867 AGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCAGGTGTCTCT 916

67 uValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsnG 84

|||||

917 GGTAAAGCGTGTGGTGGAACTGTGCCTGTGTCTCCACAAATTCGAATG 966

84 luCysGlnCysValProSerLysValThrLysLysTyrHisGluValLeu 100

|||||

967 AATGTCATGTGTCCCAAGCAAGTTACTAAAAATACCACGAGTCTCTT 1016

101 GlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThrAs 117

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117 pValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySert 134

|||||

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1117 CAGGAGGA 1124

seq\_name: /SDS8/gcdata/geneseq/geneseq/NA2000.DAT:AAA71955

seq\_documentation\_block:

ID AAA71955 standard; DNA; 1473 BP.

AC AAA71955;

XX XX

DT 19-JAN-2001 (first entry)

XX XX

DE Human VEGF-X DNA isolated from clones 4 and 7.

XX XX

KW VEGF-X; vascular endothelial growth factor; human; vulnerary; cytotstatic;

KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;

KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;

KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;

KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;

KW venous sore; diabetic ulcer; burns; skin graft growth; ds.

XX OS Homo sapiens.

XX XX

PN WO200037641-A2.

XX XX

PD 29-JUN-2000.

XX XX

PF 21-DEC-1999; 99WO-US30503.

XX XX

PR 22-DEC-1998; 98GB-0028377.

PR 18-MAR-1999; 99US-0124967.

XX PR 08-NOV-1999; 99US-0164131.

XX XX

PA (JANC ) JANSSEN PHARM NV.

XX XX

PI Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;

PI Dhanaraj SN, Xu J;

XX XX

DR WPI; 2000-442669/38.

XX DR P-PSDB; AAB10635, AAB10636.

XX XX

PT New vascular endothelial growth factor protein, useful for treating or  
 PT preventing diseases associated with inappropriate angiogenesis activity  
 PT such as cancer, rheumatoid arthritis, psoriasis and wounds -  
 XX  
 PS Claim 4; Fig 9; 127pp; English.  
 XX  
 CC This invention describes a novel vascular endothelial growth factor-X  
 CC (VEGF-X) protein (1a) and its encoding polynucleotide (11a) which has  
 CC vulnery, cytostatic, antirheumatic, antiarthritic, antipsoriatic and  
 CC antidiabetic activity and acts as an angiogenesis and vascularization  
 CC regulator. An antisense molecule of the invention is useful for treating  
 CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic  
 CC retinopathy by inhibiting angiogenic activity or inappropriate  
 CC vascularization including formation and proliferation of new blood  
 CC vessels, growth and development of tissues, tissue regeneration and organ  
 CC and tissue repair in a subject. The products of the invention are useful  
 CC for preparing medicaments for treating wounds such as dermal ulcers,  
 CC pressure sores, venous sores, diabetic ulcers and burns and to promote  
 CC skin graft growth, tissue repair, proliferation of new blood vessels,  
 CC tissue regeneration and organ repair by promoting angiogenic activity or  
 CC vascularization. This sequence encodes the human VEGF-X protein isolated  
 CC from clones 4 and 7 described in the method of the invention.  
 XX  
 SQ Sequence 1473 BP; 406 A; 321 C; 361 G; 385 T; 0 other;

alignment\_scores:  
 Quality: 754.00 Length: 136  
 Ratio: 5.544 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

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 17 apheValPheGlyArgLysSerArgValValAspLeuAsnLeuThrG 34  
 TTTTGTGTTTGGAGAAATCCAGAGTGTGGATCTGAACCTTCTAACAG 983  
 34 LuGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerIle 50  
 984 AGGAGGTAAGATTATACAGCTCACACCTCGTAACCTCTCAGTGCCTA 1033  
 51 ArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeuLe 67  
 1034 AGGGAAGAACTAAAGAGAACCGATACCAATTTCTGGCCAGGTGTCTCT 1083  
 67 uValLysArgCysGlyGlyAspCysAlaCysCysLeuHisAsnCysAsnG 84  
 1084 GGTAAACGCTGTGTGGGAAGTGTGCTGTGTCTCCAAATTCGAATG 1133  
 84 LuCysGlnCysValProSerLysValThrLysLysTyrHisGluValLeu 100  
 1134 AATGTCATGTGTCACCAAGCAAGTTACTAAAAATACCAACAGGTCCT 1183  
 101 GlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThrAs 117  
 1184 CAGTTGAGACCAAAACACCGGTGTCAGGGGATTGACAAATCACTACCGA 1233  
 117 pValAlaLeuGluHisGluGluCysAspCysValCysArgGlySerT 134  
 1234 CGTGCCCTGAGACCACTAGGAGGTGTGACTGTGTGTGTCAGAGGAGCA 1283  
 134 hrGlyGly 136  
 1284 CAGGAGGA 1291

seq\_name: /SIDS8/gcgdata/geneseq/geneseq/NA2000.DAT: AAC81582

seq\_documentation\_block:  
 ID AAC81582 standard; DNA; 1760 BP.  
 XX  
 AC AAC81582;  
 XX  
 DT 09-MAR-2001 (first entry)  
 XX  
 DE Human zveg3 DNA, SEQ ID NO:32.  
 XX  
 KW Human; zveg3; zveg3 fusion; growth factor homologue; VEGF/PDGF family;  
 KW CUB domain; PDGF-like activity; mitogenic; osteogenic;  
 KW neovascularisation; tissue repair; proliferation; differentiation;  
 KW liver damage; neuroregenerative; Alzheimer's disease; multiple sclerosis;  
 KW periodontal disease; bone fracture; wound healing; vulnery; ischaemia;  
 KW immunomodulation; hepatic; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2000066736-A1.  
 XX  
 PD 09-NOV-2000.  
 XX  
 PF 03-MAY-2000; 2000WO-US40047.  
 XX  
 PR 03-MAY-1999; 9905-0304216.  
 PR 10-NOV-1999; 9905-0164463.  
 PR 04-FEB-2000; 2000US-0180169.  
 XX  
 PA (ZYMO ) ZYMOGENETICS INC.  
 XX  
 PI Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;  
 XX  
 DR WPI: 2000-687541/67.  
 DR P-PSDB; AAB48657.  
 XX  
 PT Growth factor homologs and the nucleic acids that encode them, useful  
 PT e.g. for treating liver damage, ischemia, multiple sclerosis and  
 PT Alzheimer's disease -  
 XX  
 PS Claim 25; Page 123-125; 143pp; English.  
 XX  
 CC The invention relates to the human growth factor homologue zveg3  
 CC (AAB48653), and nucleic acids encoding it (AAC81555). zveg3 is a member  
 CC of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial  
 CC growth factor) family. zveg3 has a growth factor domain (AAB48654)  
 CC characterised by a PDGF cysteine knot structure, and a CUB domain  
 CC (AAB48655) which has a beta barrel structure. zveg3 has PDGF-like  
 CC activity, having mitogenic activity on fibroblasts, vascular smooth  
 CC muscle cells and pericytes, and has also been shown to stimulate bone  
 CC growth. The invention also relates to fusion proteins comprising human  
 CC zveg3 or fragments thereof, particularly human zveg3/human zveg3  
 CC fusions; expression constructs and host cells comprising human zveg3  
 CC nucleic acids; the recombinant expression of human zveg3; an antibody  
 CC which binds to human zveg3 or a fragment thereof; a method of activating  
 CC a cell-surface PDGF receptor using a zveg3-derived polypeptide; a  
 CC method of modulating the proliferation, differentiation, migration or  
 CC metabolism of bone cells, comprising exposing bone cells to  
 CC zveg3-derived polypeptides; and a method of detecting a genetic  
 CC abnormality in the zveg3 gene of a patient. zveg3 proteins and derived  
 CC fragments may be used to stimulate tissue development or repair, or  
 CC cellular differentiation or proliferation. They are particularly used for  
 CC the treatment or repair of liver damage, and may also be used to  
 CC modulate neurite growth (e.g., in the treatment of Alzheimer's disease or  
 CC multiple sclerosis). Due to their osteogenic activity, they may be used  
 CC in the treatment of periodontal disease and fractures. They may also be  
 CC used to enhance expansion and mobilisation of haematopoietic stem cells  
 CC and endothelial precursor stem cells, which may be useful in the  
 CC treatment of ischaemia, in wound healing, and in the modulation of the  
 CC immune system. The present sequence represents DNA encoding human  
 CC zveg3.  
 XX  
 SQ Sequence 1760 BP; 494 A; 373 C; 411 G; 482 T; 0 other;

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  Quality: 754.00      Length: 136
  Ratio: 5.544        Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

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US-09-457-066-2_COPY_210_345 x AAC81582
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17 aPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThrG 34
831 TTTTGTGTTTTGGGAAGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAG 880

34 luGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerIle 50
881 AGGAGGTAAGATTATACAGCTGCACACCTCGTAACCTCTCAGTGTCCATA 930

51 ArgGluGluLeuLysArgThrAspThrIlePheThrProGlyCysLeuLe 67
931 AGGGAAGAACTAAAGAGAACCGATACCATTTCTGGCCAGGTTGTCCT 980

67 uValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsnG 84
981 GGTAAACGCTGGTGGGAACTGTGCTGTGTCTCCAAATGCAATGCAATG 1030

84 luCysGlnCysValProSerLysValThrLysLysTyrHisGluValLeu 100
1031 AATGTCAATGTGTCCCAAGCAAGATTTACTAAAAATAACACGAGGTCTT 1080

101 GlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThrAs 117
1081 CAGTTAGACCAAGAACCGGTGTGCAGGGGATTCACAAATCACTCACCGA 1130

117 pValAlaLeuGluHisGluGluCysAspCysValCysArgGlySerT 134
1131 CGTGGCCCTGGAGCACCAATGAGGAGTGTGACTGTGTGTGCAGAGGAGCA 1180

134 hrGlyGly 136
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seq_name: /SIDS8/cgdata/geneseq/geneseq/NA2000.DAT:AAA51498

seq_documentation_block:
ID AAA51498 standard; cDNA; 1760 BP.
XX
AC AAA51498;
XX
DT 26-SEP-2000 (first entry)
XX
DE Human growth factor homologue, ZVEGF3, CDNA.
XX
KW Vascular endothelial growth factor; homologue; zveg3; CUB domain;
KW Cysteine knot; platelet-derived growth factor; PDGF; neuropilin;
KW chromosome 4q28.3; cytostatic; anti-psoriatic; anti-inflammatory;
KW anti-diabetic; ophthalmological; anti-rheumatic; anti-arthritis;
KW vulnary; ss.
XX
OS Homo sapiens.
XX
FH Key
FT CDS 154..1191
FT FT /*tag= a
FT FT /product= ZVEGF3
FT FT /*tag= b
FT FT sig_peptide 154..195
FT FT
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XX WO200034474-A2.
XX 15-JUN-2000.
XX 07-DEC-1999; 99WO-US28968.
XX 07-DEC-1998; 98US-0207120.
XX 06-JUL-1999; 99US-0142576.
XX 21-OCT-1999; 99US-0161653.
XX 12-NOV-1999; 99US-0165255.
XX (Zymo ) ZYMOGENETICS INC.
XX Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KE;
XX Gilbertson DG, West JW;
XX WPI; 2000-423420/36.
XX P-PSDB; AAY96858.
XX
XX Novel zveg3 polypeptides and nucleotides encoding them useful for
XX stimulating growth of smooth muscle cells and fibroblasts comprising an
XX epitope bearing portion of a specific amino acid sequence
XX
XX Claim 29; Page 146-148; 173pp; English.
XX
XX This cDNA encodes a human vascular endothelial growth factor homologue,
XX designated ZVEGF3. Polypeptides comprising an epitope-bearing portion
XX human or murine ZVEGF3 are claimed. The growth factors comprise a growth
XX factor domain and a CUB domain (generic sequence motifs are shown in
XX AAY96859 and AAY96860). The growth factor domain is characterized by an
XX arrangement of cysteine residues and beta-strands that is characteristic
XX of the "cysteine knot" structure of the platelet-derived growth factor
XX (PDGF) family. The CUB domain shows homology to CUB domains in
XX neuropilins, human bone morphogenetic protein-1, porcine seminal plasma
XX protein, bovine acidic seminal fluid protein and xenopus laevis
XX toll-like protein. Structural analysis and homology predict that
XX ZVEGF3 polypeptides complex with a second polypeptide to form multimeric
XX proteins. The human zveg3 gene has been mapped to chromosome 4q28.3.
XX ZVEGF3 is useful for stimulating the growth of fibroblasts or smooth
XX muscles cells, for activating cell surface PDGF-alpha receptor and for
XX inhibiting PDGF-alpha receptor mediated cellular processes. ZVEGF3 is
XX useful for regulating (post-development) organ growth, regeneration and
XX maintenance, as well as tissue maintenance and repair processes. ZVEGF3
XX antagonists are useful for treating cancer, rheumatoid arthritis,
XX diabetic retinopathy, ischemic limb disease, peripheral vascular
XX disease, myocardial ischemia, vascular intimal hyperplasia,
XX atherosclerosis, wound healing, chronic liver disease and haemangioma
XX formation. ZVEGF3 can also be used to modulate neurite growth and
XX development of the nervous system, and for treating neurodegenerative
XX diseases.
XX
XX Sequence 1760 BP; 494 A; 373 C; 411 G; 482 T; 0 other;
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  Quality: 754.00      Length: 136
  Ratio: 5.544        Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

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US-09-457-066-2_COPY_210_345 x AAA51498
Align seg 1/1 to: AAA51498 from: 1 to: 1760
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1 LeuAspLeuGluAspLeuTyrArgProThrTrpGlnLeuLeuGlyLysAl 17
781 TTGGACTTAGAAGATCTATATAGCCAACTTGGCAACTTCTTGCAAGGC 830

17 aPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThrG 34
831 TTTTGTGTTTTGGGAAGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAG 880
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34 luGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerIle 50  
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 881 AGGAGTAAAGATTATACAGCTGCACACCTCGTAACCTCTCAGTGTCCATA 930  
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 51 ArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeuLe 67  
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 931 AGGGAAGAACTAAAGAGAACCGATACCATTTCTGGCCAGGTGTCTCCT 980  
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 67 uValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsnG 84  
 |||||  
 981 GGTAAACCGCTGTGTGGGAACGTGCTGTCTCCACAATGCAATG 1030  
 |||||  
 84 luCysGlnCysValProSerLysValThrLysLysThrHisGluValLeu 100  
 |||||  
 1031 AATGTCAATGTGTCACCAAGCAAGTTACTAAAAAATACCCAGGAGTCTT 1080  
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 101 GlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThrAs 117  
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 1081 CAGTTGAGACCAAAACCGGTGTCAAGGGATTGCACAATCACTACCGA 1130  
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 117 pValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySert 134  
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 1131 CGTGGCCCTGGAGCACCATCAGGAGTGTGACGTGTGTGTGCAGAGGAGCA 1180  
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 134 hrGlyGly 136  
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 1181 CAGGAGGA 1188

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seq\_documentation\_block:

ID AAA12523 standard; cDNA; 2108 BP.

AC AAA12523;

XX 25-JUL-2000 (first entry)

XX cDNA encoding platelet-derived growth factor C (PDGF-C).

XX platelet-derived growth factor C; PDGF-C; cell proliferation;  
 KW growth factor; heparin; connective tissue; wound healing; VEGF-F;  
 KW fibroblast mitogenesis; PDGF alpha receptor activation; tumour growth;  
 KW chorlocarcinoma; Wilms tumour; megakaryoblastic leukaemia;  
 XX lung carcinoma; erythroleukemia; tissue remodelling; ss.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FH CDS 37..1073

FT /\*tag= a

FT /product= "platelet-derived growth factor C"

XX W0200018212-A2.

XX 06-APR-2000.

XX 30-SEP-1999; 99WO-US22668.

XX 30-SEP-1998; 98US-0102461.

XX 12-NOV-1998; 98US-0108109.

XX 03-DEC-1998; 98US-0110749.

XX 18-DEC-1998; 98US-0113002.

XX 21-MAY-1999; 99US-0135426.

XX 15-JUL-1999; 99US-0144022.

XX (LUDW-) LUDWIG INST CANCER RES.

XX (UYHE-) UNIV HELSINKI LICENSING LTD.

XX Eriksson U, Aase K, Lee X, Ponten A, Untela M, Alitalo K;  
 PI Oestman A, Heldin C, Betsholz C;

XX WPI; 2000-292954/25.

DR P-PSDB; AAY84557.

XX  
 PT  
 PT  
 XX

Claim 9; Fig 1; 135pp; English.

XX The present sequence encodes human platelet-derived growth factor C  
 CC (PDGF-C) (formally designated VEGF-F). PDGF-C polypeptides have the  
 CC ability to stimulate and enhance proliferation or differentiation,  
 CC and/or growth or motility of cells expressing a PDGF-C receptor.  
 CC PDGF-C polypeptides can be used in pharmaceuticals for promoting cell  
 CC proliferation, preferably in combination with one other growth factor  
 CC and heparin. Pharmaceuticals comprising PDGF-C polypeptides can also  
 CC be used for stimulating connective tissue or wound healing. The  
 CC PDGF-C polypeptide can be enzymatically processed to generate the active  
 CC truncated form of PDGF-C and used to regulate the receptor-binding  
 CC specificity of PDGF-C. PDGF-C can also be used to promote fibroblast  
 CC mitogenesis in a mammal and to induce PDGF alpha receptor activation.  
 CC PDGF-C antagonists can be used to inhibit tumour growth of a tumour  
 CC expressing PDGF-C in a mammal. Specific types of human tumours, e.g.  
 CC chorlocarcinoma, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma  
 CC and erythroleukemia, can be identified by testing for expression of  
 CC PDGF-C. PDGF-C antagonists can also be used to inhibit tissue  
 CC remodelling during invasion of tumour cells into a normal population of  
 CC cells. Antagonists can also be used to treat fibrotic conditions,  
 CC especially found in the lung, kidney or liver.

XX Sequence 2108 BP; 623 A; 400 C; 451 G; 629 T; 5 other;

alignment\_scores:

Quality: 754.00 Length: 136  
 Ratio: 5.544 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-457-066-2\_COPY\_210\_345 x AAA12523

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 17 aPheValPheGlyArgLysSerArgValValAspLeuAsnLeuThrG 34  
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 714 TTTTGTGTTTGGAGAGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAG 763  
 |||||  
 34 luGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerIle 50  
 |||||  
 764 AGGAGTTAAGATTATACAGCTGCACACCTCGTAACCTTCTCAGTGTCCATA 813  
 |||||  
 51 ArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeuLe 67  
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 814 AGGGAAGAACTAAAGAGAACCGATACCATTTCTGGCCAGGTGTCTCCT 863  
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 67 uValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsnG 84  
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 864 GGTAAACCGCTGTGTGGGAACCTGTGCTGTGTCTCCACAATGCAATG 913  
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 101 GlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThrAs 117  
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 964 CAGTTGAGACCAAAACCGGTGTCAAGGGATTGCACAATCACTACCGA 1013  
 |||||  
 117 pValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySert 134  
 |||||  
 1014 CGTGGCCCTGGAGCACCATCAGGAGTGTGACTGTGTGTGCAGAGGAGCA 1063

134 hrGlyGly 136  
|||||

1064 CAGGAGGA 1071

seq\_name: /SIDS8/gcgdata/geneseq/geneseq/NA2000.DAT:AAA71951

seq\_documentation\_block:

ID AAA71951 standard; DNA; 2475 BP.

XX AC AAA71951;

XX DT 19-JAN-2001 (first entry)

XX DE Human RACE generated VEGF-X DNA.

XX VEGF-X; vascular endothelial growth factor; human; vulnery; cytostatic;  
KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;  
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;  
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;  
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;  
KW venous sore; diabetic ulcer; burns; skin graft growth; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX CDS 122..1159

XX FT /\*tag= a

XX FT /product= "VEGF-X"

XX PN WO200037641-A2.

XX PD 29-JUN-2000.

XX XX 21-DEC-1999; 99WO-US30503.

XX PR 22-DEC-1998; 98GB-0028377.

XX PR 18-MAR-1999; 99US-0124967.

XX PR 08-NOV-1999; 99US-0164131.

XX PA (JANC ) JANSSEN PHARM NV.

XX PI Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;

XX PI Dhanaraj SN, Xu J;

XX XX WPI; 2000-442669/38.

XX DR P-PSDB; AAB10633.

XX PS New vascular endothelial growth factor protein, useful for treating or

XX PT preventing diseases associated with inappropriate angiogenesis activity  
XX PT such as cancer, rheumatoid arthritis, psoriasis and wounds -

XX PS Disclosure; Fig 6; 127pp; English.

XX CC This invention describes a novel vascular endothelial growth factor-X  
XX CC (VEGF-X) protein (Ia) and its encoding polynucleotide (Iia) which has  
XX CC vulnery, cytostatic, antirheumatic, antiarthritic, antipsoriatic and  
XX CC antidiabetic activity and acts as an angiogenesis and vascularization  
XX CC regulator. An antisense molecule of the invention is useful for treating  
XX CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic  
XX CC retinopathy by inhibiting angiogenic activity or inappropriate  
XX CC vascularization including formation and proliferation of new blood  
XX CC vessels, growth and development of tissues, tissue regeneration and organ  
XX CC and tissue repair in a subject. The products of the invention are useful  
XX CC for preparing medicaments for treating wounds such as dermal ulcers,  
XX CC pressure sores, venous sores, diabetic ulcers and burns and to promote  
XX CC skin graft growth, tissue repair, proliferation of new blood vessels,  
XX CC tissue regeneration and organ repair by promoting angiogenic activity or  
XX CC vascularization. This sequence encodes the RACE generated human VEGF-X  
XX CC protein described in the method of the invention.

XX SQ Sequence 2475 BP; 730 A; 473 C; 523 G; 749 T; 0 other;

alignment\_scores:  
Quality: 754.00 Length: 136  
Ratio: 5.544 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-457-066-2\_COPY\_210\_345 x AAA71951 ..

Align seg 1/1 to: AAA71951 from: 1 to: 2475

1 LeuAspLeuGluAspLeuTyrArgProThrTrpGlnLeuLeuGlyLysal 17  
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749 TTGGCTTAGAAGATCTATATAGGCCAACTTGGCAACTCTTTGGCAAGC 798

17 apheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThrG 34

|||||

799 TTTTGTGTTTGGAGCAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAG 848

34 luGluValArgLeuTyrSerCysThrProArgAsnPheserValserIle 50

|||||

849 AGGAGGTAAAGATTATACAGCTGCACACCTCGTAACCTTCTCAGTGTCCATA 898

51 ArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeule 67

|||||

899 AGGGAAGAACTAAAGAGAACCGATACCATTTTCTGCCAGGTTGTCTCT 948

67 uValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsnG 84

|||||

949 GGTAAACGCTGTGGTGGAACTGTGCCTGTGTCTCCACAATTCGAATG 998

84 luCysGlnCysValProSerLysValThrLysLysTyrHisGluValLeu 100

|||||

999 AATGTCAATGTGTCCCAAGCAAAAGTTACTAAAAAATACCACGAGTCTT 1048

101 GlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThrAs 117

|||||

1049 CAGTTGAGACCAAGACCGGTGTGAGGGGATTGCACAAATCACTCACCGA 1098

117 pValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySerT 134

|||||

1099 CGTGGCCCTGGAGCACCATGAGGAGTGTGACGTGTGTGTGCAGAGGGAGCA 1148

134 hrGlyGly 136

|||||

1149 CAGGAGGA 1156

seq\_name: /SIDS8/gcgdata/geneseq/geneseq/NA2000.DAT:AAA71990

seq\_documentation\_block:

ID AAA71990 standard; cDNA; 2668 BP.

XX AC AAA71990;

XX DT 19-JAN-2001 (first entry)

XX DE Human VEGF-X cDNA.

XX XX VEGF-X; vascular endothelial growth factor; human; vulnery; cytostatic;

XX KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;  
XX KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;  
XX KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;  
XX KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;  
XX KW venous sore; diabetic ulcer; burns; skin graft growth; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX CDS 267..1304

XX FT /\*tag= a

XX FT /product= "VEGF-X"

XX PN WO200037641-A2.

PD 29-JUN-2000.  
 XX  
 PF 21-DEC-1999; 99WO-US30503.  
 XX  
 PR 22-DEC-1998; 98GB-0028377.  
 PR 18-MAR-1999; 99US-0124967.  
 PR 08-NOV-1999; 99US-0164131.  
 XX  
 XX (JANC ) JANSSEN PHARM NV.  
 PA  
 XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;  
 PI Dhanaraj SN, Xu J;  
 XX  
 DR WPI: 2000-442669/38.  
 DR P-PSDB; AAB10644.  
 XX  
 PT New vascular endothelial growth factor protein, useful for treating or  
 PT preventing diseases associated with inappropriate angiogenesis activity  
 PT such as cancer, rheumatoid arthritis, psoriasis and wounds -  
 XX  
 PS Disclosure; Fig 30B; 127pp; English.  
 XX  
 CC This invention describes a novel vascular endothelial growth factor-X  
 CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has  
 CC vulnary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and  
 CC antidiabetic activity and acts as an angiogenesis and vascularization  
 CC regulator. An antisense molecule of the invention is useful for treating  
 CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic  
 CC retinopathy by inhibiting angiogenic activity or inappropriate  
 CC vascularization including formation and proliferation of new blood  
 CC vessels, growth and development of tissues, tissue regeneration and organ  
 CC and tissue repair in a subject. The products of the invention are useful  
 CC for preparing medicaments for treating wounds such as dermal ulcers,  
 CC pressure sores, venous sores, diabetic ulcers and burns and to promote  
 CC skin graft growth, tissue repair, proliferation of new blood vessels,  
 CC tissue regeneration and organ repair by promoting angiogenic activity or  
 CC vascularization. This sequence encodes a human VEGF-X protein described  
 CC in the method of the invention.  
 XX  
 SQ Sequence 2668 BP; 780 A; 511 C; 567 G; 810 T; 0 other;

alignment\_scores:  
 Quality: 754.00 Length: 136  
 Ratio: 5.544 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-457-066-2\_COPY\_210\_345 x AAA71990 ..

Align seg 1/1 to: AAA71990 from: 1 to: 2668

1 LeuAspLeuGluAspLeuTyrArgProThrTrpGlnLeuLeuGlyLysAl 17  
 |||||  
 894 TTGGACTTAGAAGATCATATAGGCCAACTTGGCAACTTCTTGGCAAGGC 943  
 |||||  
 17 aPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThrG 34  
 |||||  
 944 TTTTGTCTTTTGGAGAAATCCAGAGTGGTGCATCTGAACCTTCTTAACAG 993  
 |||||  
 34 luGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerIle 50  
 |||||  
 994 AGGAGGTAAGATTATACAGCTGCACACCTCGTAACCTCTCAGTGTCCATA 1043  
 |||||  
 51 ArgGluGluLeuLeuLysArgThrAspThrIlePheTrpProGlyCysLeuLe 67  
 |||||  
 1044 AGGGAAGAACTTAAGAGAACGATACCATTTTCTGGCCAGGTGTCTCTCT 1093  
 |||||  
 67 uValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsnG 84  
 |||||  
 1094 GGTAAACCGCTGTGGTGGAACTGTGCTGTGTCTCCAAATTCGAATG 1143  
 |||||  
 84 luCysGlnCysValProSerLysValThrLysLysTyrHisGluValLeu 100

|||||  
 1144 AATGTCATGTGTCCTCCCAAGCAAGTTACTAAAAATACCAAGAGTCTCT 1193  
 |||||  
 101 GlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThrAs 117  
 |||||  
 1194 CAGTTGAGACCAAGACCGGTGTCTCAGGGGATTGCACAAATCACTCACCGA 1243  
 |||||  
 117 pValAlaLeuGluHisGluGluCysAspCysValCysArgGlySerT 134  
 |||||  
 1244 CGTGGCCCTGGAGCACCATGAGGAGTGTGCTGTGTGCAGAGGGAGCA 1293  
 |||||  
 134 hrGlyGly 136  
 |||||  
 1294 CAGGAGGA 1301

seq\_name: /SIDSS/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA71952

seq\_documentation\_block:

ID AAA71952 standard; DNA; 2776 BP.

XX

AC AAA71952;

XX

DT 19-JAN-2001 (first entry)

XX

DE Human VEGF-X homologue DNA.

XX

KW VEGF-X; vascular endothelial growth factor; human; vulnary; cytostatic;  
 KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;  
 KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;  
 KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;  
 KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;  
 KW venous sore; diabetic ulcer; burns; skin graft growth; ds.

XX Homo sapiens.

OS

FH Key Location/Qualifiers

FT CDS 260..1297

FT

FT /\*tag= a /product= "VEGF-X homologue"

XX

PN WO200037641-A2.

XX

PD 29-JUN-2000.

XX

PF 21-DEC-1999; 99WO-US30503.

XX

PR 22-DEC-1998; 98GB-0028377.

PR

PR 18-MAR-1999; 99US-0124967.

PR

PR 08-NOV-1999; 99US-0164131.

XX

PA (JANC ) JANSSEN PHARM NV.

XX

PI Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;

PI

PI Dhanaraj SN, Xu J;

XX

DR WPI: 2000-442669/38.

DR

DR P-PSDB; AAB10634.

XX

PT New vascular endothelial growth factor protein, useful for treating or

PT

preventing diseases associated with inappropriate angiogenesis activity  
 such as cancer, rheumatoid arthritis, psoriasis and wounds -

PS

PS Disclosure; Fig 7; 127pp; English.

XX

CC This invention describes a novel vascular endothelial growth factor-X  
 CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has  
 CC vulnary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and  
 CC antidiabetic activity and acts as an angiogenesis and vascularization  
 CC regulator. An antisense molecule of the invention is useful for treating  
 CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic  
 CC retinopathy by inhibiting angiogenic activity or inappropriate  
 CC vascularization including formation and proliferation of new blood  
 CC vessels, growth and development of tissues, tissue regeneration and organ

CC and tissue repair in a subject. The products of the invention are useful  
 CC for preparing medicaments for treating wounds such as dermal ulcers,  
 CC pressure sores, venous sores, diabetic ulcers and burns and to promote  
 CC skin graft growth, tissue repair, proliferation of new blood vessels,  
 CC tissue regeneration and organ repair by promoting angiogenic activity or  
 CC vascularization. This sequence encodes the human VEGF-X protein homologue  
 CC described in the method of the invention.

XX SQ Sequence 2776 BP; 825 A; 515 C; 587 G; 849 T; 0 other;

alignment\_scores:  
 Quality: 754.00 Length: 136  
 Ratio: 5.544 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-457-066-2\_COPY\_210\_345 x AAA71952

Align seg 1/1 to: AAA71952 from: 1 to: 2776

1 LeuAspLeuGluAspLeuTyrArgProThrTrpGlnLeuLeuGlyLysAl 17  
 |||||  
 887 TTGGACTTAGAAGATCTATATAGCCCACTTGGCAAGGC 936  
 |||||  
 17 apheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThrG 34  
 |||||  
 937 TTTTGTGTTTGGAGAAATCCAGAGTGGTGATCTGAACCTCTAACAG 986  
 |||||  
 34 luCluValArgLeuTyrSerCysThrProArgAsnPheSerValSerIle 50  
 |||||  
 987 AGGAGTAAAGATTATACAGTCGACACCTCGTAACCTCTCAGTGTCATA 1036  
 |||||  
 51 ArgGluGluLeuLysArgThrAspThrIlePheThrProGlyCysLeuLe 67  
 |||||  
 1037 AGGGAAGAACTAAAGAGAACCGATACCAATTTCTGGCCAGGTGTCCT 1086  
 |||||  
 67 uValLysArgCysGlyCysAlaCysCysLysLeuHisAsnCysAsnG 84  
 |||||  
 1087 GGTAAACGCTGGTGGGAACCTGCTCTTCTCCACAATTCGAATG 1136  
 |||||  
 84 lucysGlnCysValProSerLysValThrLysLysThrHisGluValLeu 100  
 |||||  
 1137 AATGTCATATGTGTCACCAAGAAATTTACTAAAAAATACACAGAGTCTT 1186  
 |||||  
 101 GlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThrAs 117  
 |||||  
 1187 CAGTTGAGACCAAGACCGGTGTCAGGGGATTCACAAATCACTACCGA 1236  
 |||||  
 117 pValAlaLeuGluHisGluGluCysAspCysValCysArgGlySerT 134  
 |||||  
 1237 CGTGGCCCTGGAGCACCACATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCA 1286  
 |||||  
 134 hrGlyGly 136  
 |||||  
 1287 CAGGAGGA 1294

seq\_name: /SID88/gcgdata/geneseq/geneseq/NA2000.DAT:AAA52458

seq\_documentation\_block:

ID AAA52458 standard; cDNA; 2779 BP.

XX AC AAA52458;

XX AC (first entry)

XX 25-SEP-2000

XX cDNA encoding human growth factor related molecule GFRP-4.

XX Human GFRP-4; growth factor related molecule; diseased breast tissue;  
 KW bone morphogenetic protein 1; BMP-1; inflammation; immune response;  
 KW reproductive tissue; reproductive tissue; developmental disorder; cell  
 KW proliferative disorder; immune disorder; reproductive disorder;  
 KW cardiovascular disorder; bacterial infection; viral; fungal; parasitic;

KW cancer; allergy; asthma; arteriosclerosis; therapy; diagnosis; consensus;  
 KW ss.

XX Homo sapiens.

OS Location/Qualifiers  
 FH 258..1295  
 FT /\*tag= a  
 FT /product= "Human GFRP-4"

XX WO200024774-A2.

XX 04-MAY-2000.

XX 28-OCT-1999; 99WO-US25458.

XX 28-OCT-1998; 98US-0181711.

XX 11-DEC-1998; 98US-0209547.

XX 17-MAY-1999; 99US-0313457.

XX (INCY-) INCYTE PHARM INC.

XX Tang YT, Yue H, Hillman JL, Corley NC, Guegler KJ, Baughn MR;

XX Au-Young J;

XX WPI; 2000-350695/30.

XX P-PSDB; AAB03003.

XX Human growth factor related molecule protein useful for the diagnosis  
 PT and treatment of disorders associated with its activity including  
 PT developmental, cell proliferative, immune, reproductive and  
 PT cardiovascular disorders and infections -

XX Claim 9; Page 76; 80pp; English.

XX This sequence represents cDNA encoding human growth factor related  
 CC molecule GFRP-4. cDNA encoding GFRP-4 was initially identified in a  
 CC diseased breast tissue cDNA library, and the present sequence represents  
 CC a consensus derived from several overlapping and/or extended cDNA  
 CC clones. GFRP-4 has chemical and structural homology with human bone  
 CC morphogenetic protein 1 (BMP-1) (27% identity at the BMP-1 C-terminus).  
 CC GFRP-4 was found by Northern analysis to be expressed in reproductive  
 CC and cardiovascular tissue, and in cDNA libraries associated with cancer,  
 CC inflammation and the immune response. GFRP proteins (AAB03000-B03003),  
 CC nucleotides encoding them (AAA52455-A52458), GFRP agonists and  
 CC antagonists may be used to treat a wide variety of diseases associated  
 CC with increased or decreased expression or activity of GFRP proteins.  
 CC Conditions which may be treated include developmental disorders, cell  
 CC proliferative disorders (e.g., cancers), immune disorders (e.g.,  
 CC allergies, asthma), reproductive disorders (e.g., menstrual cycle  
 CC disorders), cardiovascular disorders (e.g., arteriosclerosis) and  
 CC bacterial, viral, fungal or parasitic infections. Additionally, GFRP  
 CC proteins and nucleotides can be used in the diagnosis of such disorders.

XX Sequence 2779 BP; 832 A; 515 C; 585 G; 847 T; 0 other;

alignment\_scores:

Quality: 754.00 Length: 136

Ratio: 5.544 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-457-066-2\_COPY\_210\_345 x AAA52458

Align seg 1/1 to: AAA52458 from: 1 to: 2779

1 LeuAspLeuGluAspLeuTyrArgProThrTrpGlnLeuLeuGlyLysAl 17

|||||

885 TTGGACTTAGAAGATCTATATAGCCCACTTGGCAAGGC 934

|||||

17 apheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThrG 34

|||||

935 TTTTGTGTTTGGAGAAATCCAGAGTGTGGATCTGAACCTTCTTAACAG 984  
 34 luCluValargLeuTyrSerCysThrProArgasnPheSerValSerIle 50  
 |||||  
 985 AGGAGTAAAGATTATACAGTCGACACCTCGTAACCTTCTCAGTCTCCATA 1034  
 51 ArqGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeuLe 67  
 |||||  
 1035 AGGGAAGAACTAAAGAACCGATACCATTTTCGGCCAGGTTCTCTCCT 1084  
 67 uValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsnG 84  
 |||||  
 1085 GGTAAACGCTGTGTGGGAACCTGCTCTGTCTCCACAATTGCAATG 1134  
 84 luCysGlnCysValProSerLysValThrLysLysTyrHisGluValLeu 100  
 |||||  
 1135 AATGTCAATGTGTCCCAAGCAAAAGTTACTAAAAAATACCAGAGTCTT 1184  
 101 GlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThrAs 117  
 |||||  
 1185 CAGTTGAGACCAAGACCGGTGTGAGGGGATTGCACAAATCAGTCCACGA 1234  
 117 pValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySert 134  
 |||||  
 1235 CGTGGCCCTGGACACCATGAGAGTGTGACTGTGTGTGCAGAGGGAGCA 1284  
 134 hrGlyGly 136  
 |||||  
 1285 CAGGAGGA 1292

seq\_name: /SID58/gcgdata/geneseq/geneseq/NA1999.DAT.AA223691

seq\_documentation\_block:

ID\_AA223691 standard; DNA; 2825 BP.

AC\_AA223691;

DT 11-JAN-2000 (first entry)

XX Human VEGF-E DNA.

XX VEGF-E; human; vascular endothelial cell growth factor; wound repair;  
 treatment; cardiovascular disorder; endothelial disorder; therapy;  
 tissue generation; regeneration; cardiac hypertrophy; cancer; detection;  
 angiogenic disorder; age-related macular degeneration; vascular disease;  
 neovascularization; tumor; gene mapping; ss.

OS Homo sapiens.

XX Key Location/Qualifiers  
 FH CDS 259..1296  
 FT /\*tag= a  
 ET /product= "VEGF-E"

XX WO9947677-A2.

XX 23-SEP-1999.

XX 10-MAR-1999; 99WO-US05190.

XX 17-MAR-1998; 98US-0040220.

XX 02-NOV-1998; 98US-0184216.

XX (GETH ) GENENTECH INC.

XX Ferrara N, Kuo SS;

XX WPI; 1999-580306/49.

XX P-PSDB; AAY33679.

XX New growth factor polypeptide useful for treating cardiovascular or

PT endothelial disorders, e.g. cardiac hypertrophy

XX

PS Claim 2; Fig 1; 122pp; English.

XX This invention describes the isolation of a novel human vascular  
 CC endothelial cell growth factor-E (VEGF-E) polypeptide which has  
 CC tranquilizer, vulnery and cardiac activity. VEGF-E can be administered  
 CC therapeutically, especially by expressing encoding polynucleotides, to  
 CC treat cardiovascular or endothelial disorders in mammals, especially  
 CC humans. It is useful in wound repair and tissue generation and  
 CC regeneration, and may especially be used to treat cardiac hypertrophy  
 CC It can be combined with a carrier in pharmaceutical compositions, which  
 CC can be administered to treat disorders as above. VEGF-E can be used to  
 CC screen for antagonists and agonists, and the antagonists administered to  
 CC treat angiogenic disorders in mammals (especially humans) e.g. cancer or  
 CC age-related macular degeneration. It can be used to generate antibodies,  
 CC useful therapeutically as antagonists, as above. The antibodies are also  
 CC useful to detect VEGF-E polypeptide, especially to diagnose  
 CC cardiovascular, endothelial or angiogenic disorders in mammals (e.g.  
 CC vascular disease, or neovascularization associated with tumor formation),  
 CC by contacting the antibody with a tissue sample and detecting formation  
 CC of an antibody-VEGF-E polypeptide complex. Polynucleotides encoding  
 CC VEGF-E can be used to diagnose cardiovascular and endothelial disorders  
 CC in mammals, by detecting abnormally high or low VEGF-E gene expression in  
 CC tissue samples. They can also be used to diagnose a disease or  
 CC susceptibility to a disease related to a mutated form of VEGF-E (e.g. a  
 CC cardiovascular, endothelial or angiogenic disorder such as a tumor), by  
 CC detecting a mutation in the VEGF-E-encoding sequence isolated from a  
 CC sample. They may also be used to produce probes useful to detect related  
 CC sequences or for gene mapping. This sequence encodes the human VEGF-E  
 CC protein described in the method of the invention.

XX Sequence 2825 BP; 849 A; 522 C; 605 G; 848 T; 1 other;

alignment\_scores:

Quality: 754.00 Length: 136  
 Ratio: 5.544 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-457-066-2\_COPY\_210\_345 x AA223691

Align seg 1/1 to: AA223691 from: 1 to: 2825

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 886..TTGGACTTAGAAGATCTATATAGGCCAACTTGCAACTTCTGGCAAGGC 935  
 17 aPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThrG 34  
 |||||  
 936 TTTTGTGTTTGGAGAAATCCAGAGTGTGGATCTGAACCTTCTTAACAG 985  
 34 luCluValargLeuTyrSerCysThrProArgasnPheSerValSerIle 50  
 |||||  
 986 AGGAGTAAAGATTATACAGTCGACACCTCGTAACCTTCTCAGTGTCCATA 1035  
 51 ArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeuLe 67  
 |||||  
 1036 AGGGAAGAACTAAAGAACCGATACCATTTTCTGCCAGGTTGTCTCCT 1085  
 67 uValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsnG 84  
 |||||  
 1086 GGTAAACGCTGTGTGGGAACCTGTGCTGTCTCCACAATTGCAATG 1135  
 84 luCysGlnCysValProSerLysValThrLysLysTyrHisGluValLeu 100  
 |||||  
 1136 AATGTCAATGTGTCCCAAGCAAAAGTTACTAAAAAATACCAGAGGTCCT 1185  
 101 GlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThrAs 117  
 |||||  
 1186 CAGTTGAGACCAAGACCGGTGTGAGGGGATTGCACAAATCAGTCCACGA 1235  
 117 pValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySert 134  
 |||||



1236 CGTGGCCCTGGAGCACCATTGAGGAGTGTGACTGTGTGTGCAGAGGGAGCA 1285

134 hrGlyGly 136

|||||||

1286 CAGGAGGA 1293

seq\_name: /SIDS8/gcgdata/geneseq/geneseq/NA2000.DAT:AAA47452

seq\_documentation\_block:

ID AAA47452 standard; cDNA; 2839 BP.

XX AC AAA47452;

XX XX 20-OCT-2000 (first entry)

XX DE Human TANGO 128 coding sequence.

XX KW TANGO: 128; 140; 197; 212; 213; 224; 239; modulating agent; asthma;  
KW graft versus-host diseases; rheumatoid arthritis; psoriasis;  
KW inflammatory bowel disease; septic shock; ulcerative colitis;  
KW Crohn's disease; chronic myelogenous leukemia; cancer; liver  
KW disease; Hodgkin's disease; osteoarthritis; Lyme's disease;  
KW cachexia; autoimmune disease; myasthenia gravis; autoimmune diabetes;  
KW systemic lupus erythematosus; transgenic animal; diagnosis;  
KW prognosis; prophylactic; therapeutic; human; ds.  
XX OS Homo sapiens.

XX XX Key Location/Qualifiers

XX FH 288..1325

XX FT CDS /\*tag= a

XX FT /product= TANGO 128

XX PN WO200039284-A1.

XX XX 06-JUL-2000.

XX XX 23-DEC-1999; 99WO-US31025.

XX XX 30-DEC-1998; 98US-0223546.

XX XX (MILL-) MILLENNIUM PHARM INC.

XX XX Holtzman DA;

XX XX WPI: 2000-465743/40.

XX DR P-PSDB; AAB01419.

XX PT Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213,  
PT 224 and 239 polypeptides useful for the treatment of asthma, rheumatoid  
PT arthritis, psoriasis and autoimmune diseases  
XX PS Claim 1; Fig 1; 209pp; English.

XX CC Nucleic acids encoding TANGO polypeptides are useful as modulating

CC agents for regulating cellular processes like asthma, graft

CC versus-host diseases, rheumatoid arthritis, psoriasis, inflammatory

CC bowel disease, septic shock, ulcerative colitis, Crohn's disease,

CC chronic myelogenous leukemia, cancer, liver disease, Hodgkin's

CC disease, osteoarthritis, Lyme's disease, cachexia and autoimmune

CC diseases e.g. myasthenia gravis, autoimmune diabetes and systemic

CC lupus erythematosus. The nucleic acids are also useful for producing

CC transgenic animals and the TANGO polypeptides themselves. Partial

CC TANGO-128, 140, 197, 212, 213, 224, 239 sequences are useful in

CC forensic biology, for diagnostic assays, prognostic assays,

CC pharmacogenomics and for monitoring clinical trials. TANGO

CC polypeptides are suitable for both prophylactic and therapeutic

CC methods for treating a subject at risk of a disorder or having a

CC disorder associated with aberrant TANGO expression. A wide range

CC of cellular disorders can be treated.

XX Sequence 2839 BP; 858 A; 532 C; 600 G; 849 T; 0 other;

SQ

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Percent Similarity: 100.000 Percent Identity: 100.000

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17 aPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThrG 34

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965 TTTTGTGTTTGGGAAGAAATCCAGAGTGGTGAACCTTCTTAACAG 1014

34 luGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerIle 50

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51 ArgGluGluLeuLysArgThrAspThrIlePheThrProGlyCysLeuLe 67

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67 uValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsnG 84

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1115 GGTAAACGGTGTGGTGGAACTGTGCTGTGTCTCCACAATTCGAATG 1164

84 luCysGlnCysValProSerLysValThrLysLysTyrHisGluValLeu 100

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117 pValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySerT 134

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1315 CAGGAGGA 1322

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seq\_documentation\_block:

ID AA234296 standard; cDNA; 2849 BP.

XX AC AA234296;

XX XX 07-DEC-1999 (first entry)

XX DE Human PRO200 nucleotide sequence.

XX KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;

XX KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;

XX KW secreted protein; transmembrane protein; ss.

XX OS Homo sapiens.

XX XX WO9946281-A2.

XX PD 16-SEP-1999.

XX PF 08-MAR-1999; 99WO-US05028.

XX PR 10-MAR-1998; 98US-0077450.

XX PR 11-MAR-1998; 98US-0077632.

XX PR 11-MAR-1998; 98US-0077641.

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PR 11-MAR-1998; 98US-0077649.
PR 12-MAR-1998; 98US-0077791.
PR 13-MAR-1998; 98US-0078004.
PR 17-MAR-1998; 98US-0040220.
PR 20-MAR-1998; 98US-0078886.
PR 20-MAR-1998; 98US-0078910.
PR 20-MAR-1998; 98US-0078936.
PR 20-MAR-1998; 98US-0078939.
PR 25-MAR-1998; 98US-0079294.
PR 26-MAR-1998; 98US-0079556.
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PR 21-APR-1998; 98US-0082568.
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PR 15-MAY-1998; 98US-0085669.
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PR 15-MAY-1998; 98US-0085700.
PR 15-MAY-1998; 98US-0085704.
PR 18-MAY-1998; 98US-0086023.
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PR 22-MAY-1998; 98US-0086430.
PR 22-MAY-1998; 98US-0086486.
PR 28-MAY-1998; 98US-0087098.
PR 28-MAY-1998; 98US-0087106.
PR 28-MAY-1998; 98US-0087208.
PR 30-JUL-1998; 98US-0094651.
PR 11-SEP-1998; 98US-0100038.
XX (GETH ) GENENTECH INC.
XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX WPI; 1999-551358/46.
XX P-PSDB; AAY41766.
XX
XX New secreted and transmembrane polypeptides and their polynucleotides,
XX useful for treating blood coagulation disorders, cancers and cellular
XX adhesion disorders -
XX
XX Claim 2; Fig 206; 530pp; English.
XX
XX The present invention describes secreted and transmembrane polypeptides
XX and their polynucleotides. The nucleotide sequences are useful as
XX sources of probes, primers, for chromosome mapping, and for generation
XX of antisense sequences. They can also be used to create transgenic
XX animals. The proteins can be used to treat a variety of diseases and
XX disorders, depending on their function. Diseases that may be treated
XX include blood coagulation disorders, cancers and cellular adhesion
XX disorders. They may also be used to raise antibodies. AA233891 to
XX AA234338, and AAY41685 to AAY41774 represent polynucleotide and
XX polypeptide sequence given in the exemplification of the present
XX invention.
XX
XX Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;

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    Ratio: 5.544        Gaps: 0
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1062 AGGGAAGAACTAAAGAACCAACCATTTTCTGGCCAGGTGTCTCTCT 1111
67 uValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsnG 84
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84 luCysGlnCysValProSerLysValThrLysLysTyrHisGluValLeu 100
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